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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	June 15, 2003, 18:20:48 ; Search time 1282 Seconds (without alignments) 9874.977 Million cell updates/sec
Title: Perfect score:	US-09-884-987-1_COPY_765_1199 435
Sequence:	l aagagaaaggaagtacagaaatgaaatccaaagcttggtc 435
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq Length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: 90_ba:*

2: 90_ln:*

4: 90_om:*

5: 90_ov:*

6: 90_pb:*

8: 90_pb:*

10: 90_ro:*

11: 90_sy:*

12: 90_sy:*

13: 90_un:*

14: 90_vi:*

15: em_ba:*

16: em_fun:*

17: em_lun:*

18: em_ov:*

21: em_ov:*

22: em_ov:*

23: em_pb:*

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Pred. No. is the number of results predicted: by chance to have a

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			994 H.sapiens	520 H.	1 H.	E	X83490 H.sapiens m	3 н.	16 DNA encodi	3 H.sa	0 Method fo	32 Sequence 1	30 Sequence	Š	3572		ᄗ		M67454 Human Fas a	٦	Ξ	ó	3 Sedue	AX146814 Sequence	9	œ (5 6	3542 Sequence	sapiens	ABUSI42U Macaca Ia	Macaca	Macaca	Macaca	Macaca	Œ.		AX336715 Sequence		ı v	ı U	I.sapiens	394 Human D	835	21298 Orvetol	1299	rest or less
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PRI 15-DEC-1997		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 698)	Direct Submission Submitted (24-JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,
linear		Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 698) Ruberti, G.	l Biology In
P mRNA	•	Craniata; Catarrhini	i G., Cell
698 bp 1RNA.		Chordata; Primates;	95) Rubert
HSFASCDS3 H.sapiens FAS Del3 mRNA. 247955	247995.1 GI:728580 FAS gene. Homo sapiens. Homo sapiens	Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 698) Ruberti,G.	OMISSION (24-JAN-19
HSFASCDS3 H.sapiens Z47995	247995.1 GI: FAS gene. Homo sapiens. Homo sapiens	Eukaryota; Mammalia; 1 (bases Ruberti,G.	Submitted (24-JAN
RESULT 1 HSFASCDS3 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL

ALIGNMENTS

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Ruberti,G.
Direct Submission
Submitted (24-0NN-1995) Ruberti G., Cell Biology Institute, C.N.R., Submitted (24-0NN-1995) Rome, Italy, I-00137
Immunology, viale C. Marx 43, Rome, Italy, I-00137
Z. (bases 1 to 761)
Cascino,I., Flucci,G., Papoff,G. and Ruberti,G.
Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing
J. Immunol. 154 (6), 2706-2713 (1995)
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FTQNLEGLHHDGOFCHKPCPPDVNMESSRNAHSPATPSAKRKDPDLTWGGFVFFFCQF
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Catarrhini; Hominidae; Homo.
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1. 312
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                                                                                                                                                                                                                                                                                          AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Mar 25, 1995 this sequence version replaced g1:695540.
Location/Qualifiers
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    761
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Mammalla; Eutheria; Primates;
1 (bases 1 to 761)
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FAS gene.
Homo sapiens.
Homo sapiens
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/standard_name="FAS/Apo 1"
/note="Alternative splicing variant of FAS gene missing
exons 3,4 and 6. Exon 5 translated in a different frame up
to a new stop codon at the beginning of exon 7."
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human apoptosis-inducing Fas
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Immunology, viale C.Marx 43, Rome, Italy, I-00137 2 (bases 1 to 698)

Cascino.1. Flucci.6., Papoff.G. and Ruberti.G. Three functional soluble forms of the human apoptomolecule are produced by alternative splicing 5.1 mmunol. 154 (6), 2706-2713 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="FAS/Apo 1"
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                                                                                                                                                                                                                                                                              cell_type="PHA-activated PBMC"
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367. .>698
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                                                                                                                                                                                                                                                              'clone-"FAS DEL3"
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nsras4bDL 836 bp mRNA linear PRI 30-JUN-1996
H.sapiens FAS/Apo 1 mRNA for FAS soluble protein (clone FAS
Exo4,6De1).
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ETQNLEGLHHDGQPCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R.,
Immunology, viale C.Marx 43, Rome, Italy, I-00137
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Alternative splicing variant of FAS gene missing exons 4 and 6. Exon 5 translated in a different frame up to a new stop codon at the beginning of exon 7."
                                                                                                                        Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 836)
Papoff, G., Cascino, I., Eramo, A., Starace, G., Lynch, D. H. and
                                                                                                                                                                                                                        Ruberti,G.
A N-terminal domain shared by Fas soluble variants prevents cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397. .479
/note="Not translated in this variant as there is
codon at 397."
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/note="Translated in a different frame in this
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1. .399
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                                                                                        270520.1 GI:1418815
FAS soluble protein; FAS/Apo 1 gene.
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/db_xref="taxon:9606"
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7. Immunol. (1996)
2. (bases 1 to 856)
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/number=2
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/note="Translated in a different frame in this variant up
to a new stop codon at 310."
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/note="Translated in a different frame in this variant."
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/note="Not translated in this variant."
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/note="Not translated in this variant."
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illarity 100.0%; Pred. No. 9.8e-89;
Conservative 0; Mismatches 0;
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Cheng, J., Zhou, T., Liu, C., Shapiro, J.P., Brauer, M.J., Kiefer, M.C., Barr, P.J. and Mountz, J.D.
                                                                                                  GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
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Differential expression of human Fas mRNA species upon peripheral
blood monounclear cell activation
Biochem. J. 310 (Pt 3), 957-963 (1995)
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                                                 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
                                                              GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG
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100.0%; Score 435; DB 9;
100.0%; Pred. No. 9.7e-89;
11ve 0; Mismatches 0;
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                       Length 857;
/isolate="healthy individual"
/db_xref="texon:9606"
/chromosome="10"
/map="10924.1 or 10923"
/clone="pCR TM 11.Fas delta(3,4,6)"
/cell_type="peripheral blood mononucle
391...762
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ilarity 100.0%; Pred. No. 9.7e-89;
Conservative 0; Mismatches 0;
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FAS soluble protein; FAS/Apo 1 gene.
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H.sapiens FAS/Apo 1 mRNA for FAS
Exo4Del).
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391. .637
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/gene="Fas/Apo-1"
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/gene="Fas/Apo-1"
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/gene="Fas/Apo-1"
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                 Immunology, viale C.Marx 43, Rome, Italy, I-00137
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       'translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
                                                                                                                                                                                                                                                                                                                                    ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
RCRLCDEGHDVNMESSRNAHSPATPSAKRKDPDLTWGGFVFFFCQFH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          this variant up
                                                                                                                                                                                             /note="Alternative splicing variant of FAS gene missing exon 4. Exons 5 and 6 translated in a different frame up to a new stop codon at 448."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Translated in a different frame in this variant."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 435; DB 9; 100.0%; Pred. No. 9.7e-89;
                                                                                                                                          cell_type="PHA-activated PBMC"
                                                                                                                                                                                                                                                   /evidence-experimental
/product-Fr85 soluble protein"
/protein id="CAA94430.1"
/db_xref="GI:1418818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this
Ruberti, G.
Direct Submission
Submitted (01-APR-1996) Ruberti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                          'db_xref-"SPTREMBL:Q14292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Not translated in
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                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397. .459
/note="Translated in a
to a new stop codon at
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179 c 197 g
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543. .567
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568. .>899
                                                                                                                                                                                                                                                                                                                                                                                            /evidence=experimental
                                                                                                           /db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                        "clone-"FAS Exo4Del"
                                                                                                                                                                                                                                      codon_start=1
                                                                                                 /isolate="LN"
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/number=2
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Matches 435; Conservative
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H.Sapiens mRNA for Fas/Apo-1 (clone pCRTM11-Fasdelta(3,4)).
X83490
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 920)
Cheng, J., Zhou, T., Liu, C., Shapiro, J.P., Brauer, M.J., Klefer, M.C., Barr, P.J. and Mountz, J.D.
                                                                                                300
                                                                                                                       301 TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 360
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Direct Submission
Submitted (14-DEC-1994) J. Cheng, University of Alabama at
Submitted (14-DEC-1994) J. Cheng, University of Alabama at
Birmingham, Division of Clinical Immunol. & Rheum., UAB Station,
LHRB 473, Birmingham AL 35294-0007, USA
3 (bases 1 to 920)
Liu,C., Cheng, J. and Mountz, J.D.
                                                                                                241 GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG
                                                                                                                                                                                                                          /organism="Homo sapiens"
//isolate="healthy individual"
/db_xref="taxon:9606"
/chromosome="10"
/map="1043.1 or 10q23"
/clone="pCR TW 11-Fas delta(3,4)"
/cell_type="peripheral blood mononuclear cells"
391 .637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protection from Fas-mediated apoptosis by
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Biochem. J. 310 (Pt 3), 957-963 (1995)
96013198
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ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
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SNTKCKEEVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGV
MTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKD
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; Pred. No. 9.6e-89;
0; Mismatches 0;
             /evidence=experimental
/product="FAS soluble protein"
/protein_id="CAA88031.1"
                                                                                                                                                                        /standard_name="FAS/Apo 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="FAS/Apo 1"
/number=9
                                                                /db_xref="SPTREMBL:014293"
                                                                                                                                                                                                                            /standard_name="FAS/Apo 1"
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506. .588
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589. 613
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                                                    /db_xref="GI:695539"
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Matches 435; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-JAN-1995)/Ruberti G., Cell Biology Institute, C.N.R., Immunology, viale C.Marx 43, Rome, Italy, I-00137
2 (bases 1 to 945)
                                                                                                                                                                                                                                                                                                                                              649 TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 708
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Catarrhini; Hominidae; Homo.
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/note="Alternative splicing variant of FAS gene missing
exon 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unree functional soluble forms of the human apoptosis-inducing molecule are produced by alternative splicing J. Immunol. 154 (6), 2706-2713 (1991)
                                                                TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
                                                  1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
                           Gaps
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Length 920;
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Score 435; DB 9;
Pred. No. 9.6e-89;
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                        Mismatches
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 945)
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247993
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100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCAAAGCTTGGTC 435
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                          Conservative
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            Similarity
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        Best Local Sim
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Query Match
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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HSFASCDS1
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PRI 28-NOV-1995
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                                 361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA 420
                                                  871 TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 930
                                                                                                                                                                                                                                                                                                                                                                                         Cheng,J., Zhou,T., Liu,C., Shapiro,J.P., Brauer,M.J., Klefer,M.C.,
Barr,P.J. and Mountz,J.D.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1104)
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Submitteed (14-DEC-1994) J. Cheng, University of Alabama at Birmingham, Division of Clinical Immunol. 6 Rheum., UAB Station, LHRB 473; Birmingham AL 35294-0007, USA

3. Chaess 1 to 1104)

1. Liu, C., Cheng, J. and Mountz, J.D.

Differential expression of human rask many as pecies upon periphera Blochem. J. 310 (Pt 3), 957-993 (1995)
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/clone="pCR TM.11-Fas delta TM"
/cell_type="peripheral blood mononuclear cells"
700 .762
/gene="Fas/Apo-1"
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1larity 100.0%; Pred. No. 9.5e-89;
Conservative 0; Mismatches 0:
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/db_xref="taxon:9606"
/chromosome="10"
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/gene="Fas/Apo-1"
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Cheng, J.
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808 TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAAAATT 867
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Key Location/Qualifiers
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strandedness: Double;
topology: Linear;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1 205 c 217 g 24:
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14-FEB-1992 JP 1992028090
SSADA JUICHT
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PATENT: JP 199311959-A (2 3
OSAKA BIO SCI. KENKVUSHO
OS HOMO SAPIENS (HUMARA)
PN JP 1993219959-A/2
                                                                                                421 ATCCAAAGCTTGGTC 435
                                                                                                                   928 ATCCAAAGCTIGGTC 942
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Osada, J.
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JP 1993219959-A/2.
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if the Fas (APO-1) antigen, Fas.DELTA.TM
29-JUL-1997;
1120 GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGGGG
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Sequence 18 from patent US 5652210.
IS8632.
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Barr, P.J., Shapiro, J.P. and
Soluble splice variant of th
Patent: US 5652210-A 18 29-J
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309 c 340 g
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Method for inducing apoptosis.
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JP 2000102389-A/7.
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                                                                  PROTECTION OF USEFUL IMMUNE
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                                                                                                                                                                                                              Score 435; DB 6
Pred. No. 9e-89;
                                       1 (bases 1 to 2534)
Screaton, G.R. and Xu, X.
MATERIALS AND METHODS RELATING TO-THE
                                                                                                                                                                                                                                      Mismatches
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1 (bases 1 to 2534)
Nagata,S., Itoh,N., and Yonehara,S.
DNA coding for human cell surface al Patent: US 6270998-A 1 07-AUG-2001;
Location/Qualifiers
                                                                                        Patent: WO 9835692-A 4 20-AUG-1998;
SCREATON GAVIN ROBERT (GB); ISIS IN
LOCATION/QUALIFIERS
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/db_xref="taxon:32644"
1487 c 503 g 727
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Sequence 1 from patent US 6270998
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487 c 503 g
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Best Local Similarity 100.0%;
Matches 435; Conservative (
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AR163572
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PAT 07-0CT-1997
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Barr, P.J., Shapiro, J.P. and Kiefer, M.C.
Recombinant production of a coluble pplice (Apo-1) antigen, fas TM
Patent: US 5663070-A 18 62-SEP-1997
Location/Qualifiers
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100.0%; Pred. No. 9e-89;
tive 0; Mismatches (
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Sequence 18 from patent US 5663070.
I63530
I63530.1 GI:2481103
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Sequence 4 from Patent W09835692.
A87646
A87646.1 GI:6736281
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474 c 489 g
                                   ATCCAAAGCTTGGTC 435
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Best Local Similarity 100.
Matches 435; Conservative
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GCAGAACAGAAAGTICAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGGG 1064
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Score 435; DB 6
Pred. No. 9e-89;
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Pred. No. 9e-89;
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                 Sequence 16 from patent US 6306395. ARI73438
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487 c 503 q
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Location/Qualifier
1. .2534
                                                                                                             1 (bases 1 to 2534)
Nakamura, N. and Nagata, S.
Fas antigen derivatives
                                                     AR173438.1 GI:17913758
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Local Similarity 100.0%;
les 435; Conservative 0
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Matches
RESULT 15
AR173438
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1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT

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                         GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG
                                                              TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence #9 used t	Human Fas soluble	Human cDNA differe	Human Fas soluble	Human Fas antigen	Apoptobody3sc fusi	Fas-delta-TM cDNA.	Soluble Fas recept	Human cell surface
SUMMARIES	ΩI	ABN79685	AAT34529	ABK84693	AAT34527	AAT34526	AAA39167	AAQ93879	AAX24878	AAQ29959
	DB	24	17	24	17	17	21	16	20	13
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09-MAR-2001; 2001US-0802669. 12-APR-1999; 99US-0290640. 18-SEP-2000; 2000US-0665615.

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)	20	33.	9.66			AAT34530		Human Fas soluble
	21	33	9.66			AAA91129		CD44HextraFAStm/cy
	22	33	9.66			AAA91130		CD44Hextra/tmFAScy
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	35	67	38.5			AAT16305		
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                                                                                                                               Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand or Fas associated protein-1 is useful for inhibiting expression of Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGAACAĠAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG
                                                                                                                                                                                                                                                                            antinfianmatory, hepatotropic, or transmissupplessare, antinfianmatory, hepatotropic. Antisense oligonuclectides were designed to target human Fas. Oligonuclectides were synthesised as chimeric oligonuclectides and are useful for treating an animal having an autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition associated with apoptosis, allograft rejection, or ischemia reperfusion injury. Optionally, the above mentioned conditions are prevented by contacting the allograft with the antisense oligonuclectides are used in diagnostics, therapeutics, prophylaxis and as research reagents and in kits. The oligonuclectides are also useful for research purposes. The present nucleotide sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                Fas ligand, or Fas associated protein-1 (Fap-1). The inhibition Fas mediated signalling is thought to be immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 435; DB 24; Length 836; 100.0%; Pred. No. 1.8e-108; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                    This invention relates to an antisense compound encoding Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 836 BP; 297 A; 166 C; 183 G; 190 T; 0 other;
                                                              Zhang H;
                                                                                                                                                                                                       Example 18; Page 67-68; 84pp; English.
                                                           Wyatt J,
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Matches 435; Conservative
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(MARC/) MARCUSSON E (WYAT/) WYATT J.
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P-PSDB; \ABP35574.
                                                           Márcusson
                              ZHANG H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 Human Fas cDNA variants (AA734527-30) are derived from alternative splicing of Fas gene transcripts. They were identified following PCR amplification of CDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angloimmunoblastic lymphadenopathy (ALLD) patients and from healthy subjects. In comparison to the Fas gene (AA734526), variant Fas del3 (AA734529) has a deletion of nucleotides 391-637. This deletion causes frame shifting and an altered amino acid sequence (AAR99683).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
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                                  angioimmunoblastic lymphadenopathy; AILD; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natural, soluble form of Fas antigen secreted by human cells is result of alternative mRNA processing – used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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100.0%; Pred. No. 1.9e-108;
ative 0; Mismatches 0;
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Human Fas soluble antigen Fas del3 cDNA
                                                                                                                                                     Location/Qualifiers
26..307
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74.tag a
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Best Local Similarity
Matches 435; Conserv
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                                                                                                              Homo sapiens
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AAT34529 RESULT

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA detecting the level of expression of gene(s) (Gs) identified by the expression level in an unactivated comparing the expression level in an unactivated comparing the expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of Ga is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that the expression of Ga is a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the subject to a pathogen or sterile inflammatory disease, by detecting the subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where
GCAGAACAGAAAGTICAACIGCITCGIAAIIGGCAICAACTICAIGGAAAGAAAGAAGG 300
                                                                                                    GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGAGCG 648
                                                                                                                                                             361 CAGACTATCATCCTCCAAGGACATTACTAGTGACTCCAGAAAATTCAAAACTTCAGAAATGAA 420
                                                                                                                                                                                TATGACACATTGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTTGCAGAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatold arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcertive colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA differentially expressed in granulocytic cells #1264
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                                                                                                                                                                                                                                                                                                                                                                                       ABK84693 standard; cDNA; 920 BP
                                                                                                                                                                                                                                            421 ATCCAAAGCTTGGTC 435
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the level of expression of the gene is indicative of inflammation;

(4) treating (M5) an inflammation (especially chronic) or in a tissue,

con allegid response in a subject, exposure of a subject to a pathogen

or sterile inflammatory disease, by contacting a tissue having

inflammation with an agent that modulates the expression of gene(s)

con fine tissue. Mi is useful for detecting GGA; M2 is useful for

modulating GA; M3 is useful for screening an agent capable of modulating

GA preferably in an inflammation in a tissue; M4 is useful for

GA preferably in an inflammation of a subject to a pathogen or sterile

confercting an inflammation (especially chronic) in a tissue, an allergic

response in a subject, exposure of a subject to a pathogen or sterile

confercting an inflammation (especially chronic) in a tissue, an allergic

response in a subject, exposure of a subject to a pathogen or sterile

conferction phritis, asthma, thrombosis, cardiac reperfusion injury, RRDS, adult respiratory distress syndrome,

conferction phritis, asthma, thrombosis, cardiac reperfusion injury, renally periodontal disease; also bacterial infection, viral infection,

conferction, protozoal infection, fungal infection and M5 is

consequence represents a gene differentially expressed in granulocytes.

conferction printed specification, but was obtained in electronic

format directly from WIPO at

conference and precedence and precedence and precedence format direction in the printed precedence and precedence and precedence format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 920 BP; 312 A; 180 C; 186 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; DB 24; I
NB, Pred. No. 1.9e-108;
O; Mismatches O: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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Best Local Similarity 100.
Matches 435; Conservative
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100.0%; Pred. No. 2e-108;
ive 0; Mismatches 0
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26..1033
                                                                                                                                                                                                          AAT34526 standard; cDNA; 1167 BP
                                                                                      ATCCAAAGCTTGGTC 435
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/*tag= c
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P-PSDB; AAR99681.
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Best Local Similarity
Matches 435; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 Human Fas cDNA variants (AAT34527-30) are derived from alternative splicing of Fas gene transcripts. They were identified following PCR amplification of cDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angioimmunoblastic lymphadenopathy (ALLD) patients and from healthy subjects. In comparison to the Fas gene (AAT34526), variant Fas dell (AAT34528) lacks nucleotides 700-762 as a result of an exon deletion. The encoded protein (AAR99681) lacks the transmembrane region of insoluble Fas antigen (AAR99681). The cDNA can be used for prodn. of recombinant, soluble dell variant or as a specific probe.
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100.0%; Pred. No. 2e-108;
tive 0; Mismatches 0;
angioimmunoblastic lymphadenopathy; AILD; ss
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                                                                 Location/Qualifiers
26..970
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Conservative (
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P-PSDB; AAR99682.
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es 435; Conserv
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                                   Homo sapiens
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                                                                                                                                                                       Apoptobody3sc fusion protein encoding nucleotide sequence SEQ ID NO:7.
                                            AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGA
                                                                                           TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
       GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
                                                                AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
                                                                                                                       GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCG
                AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
                                                                                                                                                                                                                                                                                                                                                                                    fusion gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises transfecting fused gene to cell and
                                                                                                                                                                                                                                                                                                                                                                                   Human; Fas antigen; apoptosis; apoptobodyjsc; antibody; fi
medical; pharmaceutical; pharmacological; biochemical; ds
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(HAGI/) HAGIWARA H
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Synthetic.
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transfected to a cell to express the fused gene and then an idlotype antibody is reacted with the expressed cell. The method is useful in medical, pharmacoutical, pharmacological and blochemical fields. The present sequence encodes a fusion protein designated apoptobodyisc, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                       Length 1457;
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                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                     Sequence 1457'BP; 441 A; 309 C; 340 G; 367 T; 0 other;
                                                                                                                                                                                                                  Query Match 100.0%; Score 435; DB 21; Best Local Similarity 100.0%; Pred. No. 2.2e-108; Matches 435; Conservative 0; Mismatches 0;
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/*tag= /b
243..1136
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702 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This present sequence is a DNA clone encoding soluble Fas receptor (see AAW98070). The invention provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Fas ligand (Fast). In some embodiments, Fast is coadministered with the immunosuppressive agent, and the cell mixture comprises neutrophil cells. The method can be practised in vitro, ex vivo on the coadministry of the coad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neutrophil cells. The method can be practised in vitro, ex vivo in vivo. Suitable immunosuppressive agents include antisense no vivo. Suitable immunosuppressive agents include antisense molecules that inhibit endogenous Fasi expression, soluble Fasi receptors, ribozymes that inhibit the endogenous expression of Fasi, drugs that inhibit Fasi signalling, agents that induce the endogenous expression of transforming growth factor (TGF)-beta, and polynucleotides coding for an immunosuppressive agent such as TGF-beta. The method can be used for treating diseases associated with an undesired Fasi-mediated proinflammatory response, e.g. graft versus host disease, or an autoimmune disease such as
rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systemic lupus erythematosus, rheumatoid arthritis and psoriasis. The invention also provides a method for identifying agents which modulate FasL stimulation of a proinflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibition of proinflammatory responses - using an agent which modulates FasL stimulation, used for treating graft versus host
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/transl_except= (pos:519..521, aa:Gly)
195..242
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ilarity . 100.0%; Pred. No. 2.6e-108;
Conservative 0; Mismatches 0;
                                                                                                                        Location/Qualifiers
195..1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease or autoimmune disease
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2455..2460
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243..1136
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Best Local Similarity
Matches 435; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                     mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.
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                                                                                                                                                                                                                                                                                                                                         claim 3; Fig.3-1 to 3-4; 38pp; English.
                                                                                                                     Shapiro JP;
                                                                     (LXRB-) LXR BIOTECHNOLOGY INC.
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                                                                                                                   Barr PJ, Kiefer MC,
                                                                                                                                                                 1995-200120/26
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                    15-NOV-1993;
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Length 2471; Indels 9

27pp; English

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A CDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The CDNA was ligated to BerXI-cut vector pCEV4 via BstXI linkers. The KT3 CDNA library was used to transfect monkey COS 7 cells which were "panned" in buffer containing murine anti-Fas Ab. The cells were "panned" on plates pre-coated with goat anti-mouse antibodies. The Fas-expressing cells adhered to the plates.

Extrachromosomal DNA was prepared from adhered cells and used to transform E.coli VMIO0 cells. A 520bp XhoI-BamHI fragment from a positive clone (pF3) was used to screen the KT-3 cDNA library. The longest cDNA clone was designated pF58 and contains an ORF correspond to a 35 amino acid pre-protein and a 319 amino acid mature protein
                                                                                                                                           (i.e. human Fas antigen).
        Claim 3; Fig 1 and 2;
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       AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
                                                                                                                     TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAAAATT 360
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                                                        882 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 941
                                                                              GCAGAACTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residue is not present in
                                                                                                                                                                                                                                                                                                                                                             Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.
                                                                                                                                                                                                                                                                            AAQ29959 standard; cDNA to mRNA; 2534 BP
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/product= Fas_antigen
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195..242
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                                                                                                                                                                                                                                                                                                                                       Human cell surface antigen.
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P-PSDB; AAR28084.
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                                Length 2534;
                                                                 Indels
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Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                Score 435; DB 13;
Pred. No. 2.6e-108;
                                                               Mismatches
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195..1202
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ilarity 100.0%;
Conservative 0
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es 435; Conserv
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AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
                                                             Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
                                      hFas doding sequence from plasmid pCEV4/hFas.
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Hachiya T, Noguchi J,
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-087635/09.
P-PSDB; AAR92528.
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06-JUL-1994;
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                                                                                                                                                                                                                Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                       AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of
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                                                                                                                                                                                                                                                                                                                                                                     Score 435; DB 16;
Pred. No. 2.6e-108;
Mismatches 0;
                                                                                                                                                                                                                                                  Example 1; Pages 15-17; 51pp; Japanese
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100.0%;
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243..1199
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ses 435; Conservative
195..242
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P-PSDB; AAR78606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
(NISB ) JAPAN TOBACCO INC.
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Jocation/Qualifiers
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94JP-0154706
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CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus;
simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
                                                                                                                           Length
                                                                                                                                                            Indels
                                                                                       Sequence 2534 BP; 81.7 A; 491 C; 499 G; 727 T; 0 other;
                                                                                                                        100.0%; Score 435; DB 18;
100.0%; Pred. No. 2.6e-108;
ive 0; Mismatches 0;
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                                                      virus-infected cells.
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                                                                                                                           Query Match
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                                                                                                                                                              Matches
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                                                                                                                          AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA
                                      TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
                                                                                                                                                                             CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAAACTTCAGAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas antigen derivative containing modified extracellular region - has low antigenicity, promotes apoptosis and is useful in treatment of viral and other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis regulation; gene therapy;
lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the lst cysteine residue (preferably at least 29 residues are deleted). The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use
                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                         to mRNA; 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= Fas_antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Flg 1-2; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
195..1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Fas antigen; derivative;
treatment; diabetes; arthritis;
                                                                                                                                                                                                                                                                                 ATCCAAAGCTTGGTC 1199
                                                                                                                                                                                                                                                ATCCAAAGCTTGGTC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOCH ) MOCHIDA PHARM CO LTD (OSAB-) OSAKA BIOSCIENCE INS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-JP01502.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195..242
/*tag= b
243..1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis modulation; ss.
                                                                                                                                                                                                                                                                                                                                                                     AAV07002 standard; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Fas antigen cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-558981/51.
P-PSDB; AAW50289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
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                                                                                                                                                                                                                                                                                                                                      RESULT 12
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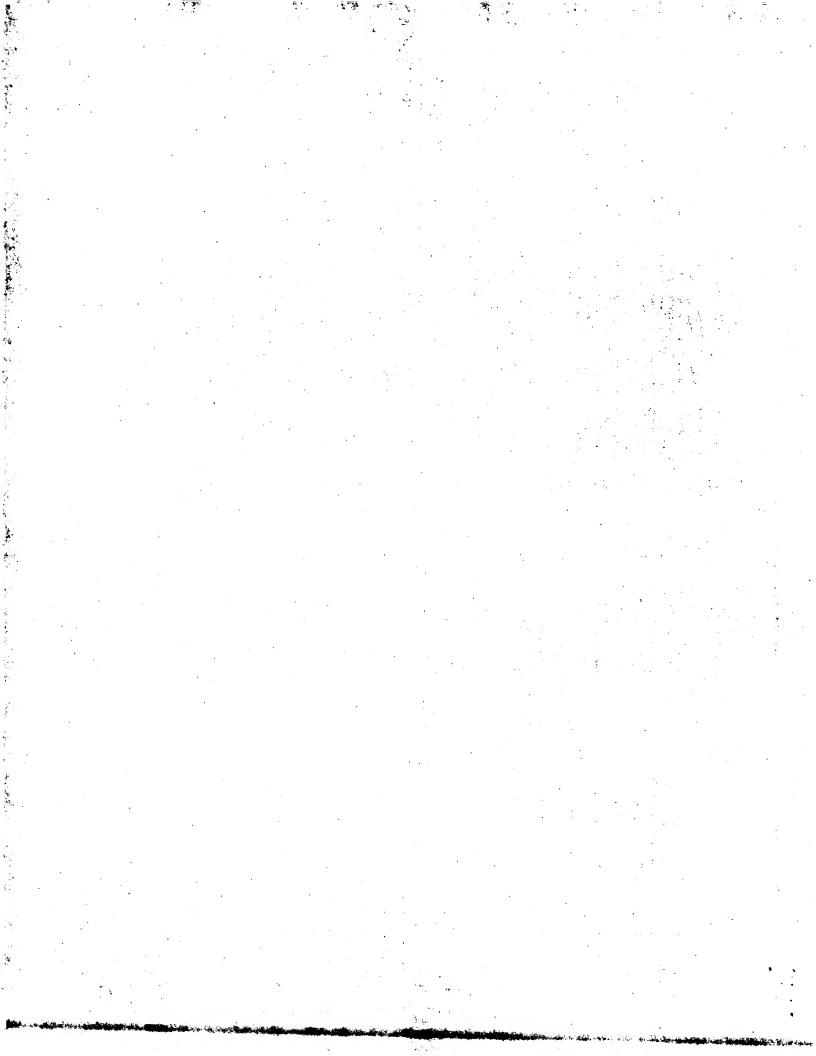
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Homo sapiens
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                                                                                                                                                                AAC61798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAAAATT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis of lymphocytes can be triggered by the interaction of the cell surface receptor Fas and its ligand Fas. By interfering with this interaction, the method described and its preparations can prevent apoptosis of CD8+ TK lymphocytes caused by expression of Fasi. on activated CD4+ cells. Such Fasi-expressing activated CD4+ cells are especially the result of CD4+ cell infection with an immunodeficiency virus e.g. human immunodeficency virus (SIV). The claimed prevention of apoptosis may then allow annihumance/Fegeneration of cytocoxic T lymphocyte (CT1) activity towards the CD4+ cells infected with the infectious agent, enabling treatment (prophylactic and/or therapeutic) of immunodeficiency
                                                                                                                                                                                                                                                                                                         method of the invention. The method is concerned with reducing depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK) cells in an immune cell population which also comprises of Fas-ligand (FasL)-expressing activated CD4+ cells. It involves contacting this immune cell population with an effective amount of an agent (e.g. a soluble Fas-Fc fusion protein) which would interfere with the interestion between Fas and FasL. Therefore, the method is useful for identifying suitable agents which can reduce depletion of activated Fas-expressing CD8+ TK cells in immune cell populations. Also claimed is the use of the agent in the manufacture of therapeutic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                    Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
                                                                                                                                                                                                                                                                                              sequence represents a Fas cDNA sequence used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 435; DB 19;
100.0%; Pred. No. 2.6e-108;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                Disclosure; Fig 10; 71pp; English.
                                                                       97GB-0003276
                                          98WO-GB00485
                                                                                                    (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                             WPI; 1998-456867/39.
P-PSDB; AAW49104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                   X nX
                                                                                                                                 Screaton GR,
                                          17-FEB-1998;
                                                                       17-FEB-1997;
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method of th
             20-AUG-1998
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Matches
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361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAAACTTCAGAAATGAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
Fas associated protein 1; protein tyrosine phosphatase; cancer;
autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligand (RasL), or Fap-1 (Fas associated protein 1, protein tyrosine phosphatase). The antisense compounds are used to inhibit the expression of Fas. FasL or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 435; DB 21; Best Local Similarity 100.0%; Pred. No. 2.6e-108; Matches 435; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 71-73; 116pp; English.
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221..1228
                                                                                                                                                                                                                                                                                                                                                           AAC61798 standard; DNA; 2551 BP
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/product= "Fas"
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                                                                                                                              421 ATCCAAAGCTTGGTC
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                               180
                                       AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACA'CA 240
                                                                                             360
                                                                                                                                                           420
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand or Fas associated protein-1 is useful for inhibiting expression fas, Fas ligand, or Fap-1 in cells or tissues, and for treating hepatitis
                                                                                                     CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA
GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
              851 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAAATTTATCTGATGTTGACTTGAGT
                                                                                                                            TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
                               AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
                                                                                                                                                                                                                                                                                                                        tostatic; vasotropic; hepatitis; cancer; allograft rejection;
                                                                                                                                                                                                                                                                                                               Human; immunosuppressive; antiinflammatory; hepatotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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MARCUSSON 1
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ZHANG H.
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                  Pas ligand, or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated signalling is thought to be immunosuppressive, antinflammatory, hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were designed to target human Fas. Oligonucleotides were synthesised as chimeric oligonucleotides and are useful for treating an animal having an autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition associated with apoptosis, allograft rejection, or ischemia reperfusion injury. Optionally, the above mentioned conditions are prevented by contacting the allograft with the antisense oligonucleotide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                  oligonuclectides are used in diagnostics, therapeutics, prophylaxis and as research reagents and in kits. The oligonuclectides are also useful for research purposes. The present nucleotide sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                             This invention relates to an antisense compound encoding
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Page 25-27; 84pp; English.
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Job time : 219 secs
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Matches 435; Conservative
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US-08-560-231-26
US-09-080-704A-26
US-08-235-218-2
US-08-714-918-18
US-09-265-315-18
US-09-265-315-18
US-09-266-417-18
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US-08-206-188B-35
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PRICE APPLICATION DATE: APPLICATION NUMBER: USSN 08/371,263 FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
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US-08-152-443A-18
US-08-152-443A-18
US-08-152-443A-18
US-08-19-231-18
US-09-190-100-16
US-09-290-640-1
US-09-290-640-65
US-08-559-896B-1
US-08-559-896B-1
US-08-61-156A-20
US-08-61-156A-20
US-08-61-527-68
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuc
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Best Local Similarity 100.0%; Pred. No. 3.2e-109;
Matches 435; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          SECRETED HUMAN FAS ANTIGEN
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
INFORMATION FOR SEG ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED HUMAN FA
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                             Sequence 7, Application PC/TUS9517083 GENERAL INFORMATION: APPLICANT:
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                                                          ATCCAAAGCTTGGTC 435
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PCT-US95-17083-7
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3.4e-109;
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                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                       Score 435;
Pred. No. 3
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
                                                     JMBER: PCT/US95/17083
CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     100.0%; Scu.
100.0%; Pre
0;
                                                                                                                                              INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1104 base pairs TYPE: nucletc acid STRANDEDNESS: single
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FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TITLE OF INVENTION: SECR NUMBER OF SEQUENCES: 16 CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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Best Local Similarity
Matches 435; Conserv
                                                                                            CLASSIFICATION:
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                                                                         FILING DATE:
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STRANDEDNESS
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PCT-US95-17083-3
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APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                    Score 435; DB 1; 1
Pred. No. 4.4e-109;
Mismatches 0;
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Patent No. 5663070
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100.0%; Pri
              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
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                            (415) 813-5600
(415) 494-0792
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                                         TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
LYPE: nucleic acid
STRANDEDNESS: single
 REFERENCE/DOCKET NUMBER:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
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Best Local Similarity
Matches 435; Conserv
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FEATURE:
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                                                                                                                                                                                  LOCATION:
FEATURE:
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US-08-444-231-18
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APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
ATILLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
SITRET: 755 Page Mill Road
CITY: Palo Alto
                                       Length 1167;
                                                                     Indels
                                         100.0%; Score 435; DB 5; I
100.0%; Pred. No. 3.4e-109;
iive 0; Mismatches 0;
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FILING DATE: 15-NOV-1993
ATTORNEY AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444/2:
FILING DATE: 18 MAY-1995
CLASSIFICATION: 530
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REGISTRATION NUMBER: 33
                                         Query Match
Best Local Similarity 100.
Matches 435; Conservative
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APPLICATION NUMBER: 1
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; TOPOLOGY:
PCT-US95-17083-1
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APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
                                                                                                                               ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
                       NAGATA, Shigekazu
                                                                                               NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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LOCATION:
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                                                                                                                                                                                                                   COUNTRY:
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                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version/#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 435; DB 1; I
Best Local Similarity 100.0%; Pred. No. 4.4e-109;
Matches 435; Conservative 0; Mismatches 0;
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-2006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
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                                     Floppy disk
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LOCATION: 243
               READABLE FORM:
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LOCATION: 195..1136
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                                   MEDIUM TYPE:
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US-08-152-443A-18
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Application US/08219237B

US-08-219-237B

RESULT 7

Sequence 1, Patent No. !

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to an established consensus
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                      SOFTWARE: Datentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR///
                                                                                               ....ен: US/08/219,237B
28-MAR-1994
8: Аэг
                                                                                                                                                                                                 APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA ORIGINAL SOURCE: ORGANISM: Homo sapiens
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ATYORNEY, AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28, 8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 2534 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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195..242
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 2352..2357
IDENTIFICATION METHOD:
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                                                                                                                                         FILING DATE: 28 CLASSIFICATION:
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SEQUENCE CHARACTERISTICS:
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                                     Gaps
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          Length 2534;
                                  Indels
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APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STRRET: P.O. BOX 747
CITY: FALLS CHURCH
            Score 435; DB 2; I
Pred. No. 4.5e-109;
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100.0%; Scc. No. ...
100.0%; Pred. No. ...
0; Mismatches
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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6270998
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NAME: MUREHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/COCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           1185 ATCCAAAGCTTGGTC 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                              421 ATCCAAAGCTTGGTC 435
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MEDIUM TYPE: Floppy disk
                      435; Conservative
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ZIP: 22040-0747
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GENERAL INFORMATION
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          Query Match
Best Local S
Matches 435
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APPLICANT: NAKAPURA.
APPLICANT: HAKAPURA.
APPLICANT: HAKAPUR.
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
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100.08;
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            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
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2534 base pairs
                                                                                        Homo sapiens
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243..1199
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195..242
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1831:.1836
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2352..2357
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2518..2532
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195..1202
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LOCATION:
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LOCATION:
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Matches 435;
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Pred. No. 4.5e-109;
0; Mismatches 0;
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100.0%; Pred. No. 3.1e-87;
iive 0; Mismatches 0;
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                                           DATE: 1992-05-25
DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
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APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
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                                                                                                                            100.0%;
100.0%;
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LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                             Ouery Match 100.
Best Local Similarity 100.
Matches 435; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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Matches 354; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                          PAGES: 10709-10715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
PCT-US95-17083-5.
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                                                                                           US-09-290-640-1
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APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REFERENCE: ISPH-0351
                                                                                                                                                                                                                                                                                                                                       824
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                                                                                                                                                                                                                                    Length 2534;
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                                                                                                                                                                                                                                  ; Score 435; DB 4; I; Pred. No. 4.5e-109; 0; Mismatches 0;
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT PAPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
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Best Local Similarity 100.
Matches 435; Conservative
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LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOHNNAL: J. Biol. Chem.
VOLUME: 267
                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-180-100-16
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                                                                                                                                              LENGTH: 2534
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LENGTH: 2551
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                                                                863 TGCTGGTACCAATCTCATGGGAAGAGTGATGCATATCAAGATTTAATCAAGGGTCTCAAA 922
                                        AAAGCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATCATCCTCAAGGACATTACT 387
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Pred. No. 0.00015;
0; Mismatches 141; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
TUMBER OF SEQUENCES: 52
CORRESPONDENCE - ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1800 Diagonal Road, Suite 500
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                                                                                                                                                                                                                                                                   Sequence 14, Application US/08232463 Patent No. 5670367
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Best Local Similarity 4.2%; Pre
Matches 15; Conservative 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 22313-0299
COMPUTER READABLE FORM:
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                    US-08-232-463-14/c
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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
CURRENT FILE REPERENCE: ISPH-0351
CURRENT PRILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFWWARE: Patentin Ver. 2.0
SEQ ID NO 65
                                                                                                                                                                                                                                                                   683 ATACCAATGAATGCTCAAATCTTAGCTTGAGTAAATACATCCCGAGAATTGCTGAAGAC 742
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                                                                                                    202 AAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAAGTTCAACTG 261
                                                                                                                                                                                      CTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCGTATGACACATTGATTAAAGAT 321
                     GGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCAATGAAGCC 201
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                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/09290640
Patent No. 6204055
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PUBLICATION INFORMATION:
JOURNAL: J. Immunol.
VOLUME: 148
PAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LOCATION: (50)
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AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
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388 AATAATATGAATAGTGATCAAGTTGATAAAATACATAGAGAAGAATTAGAAAAAATCGAA 447
                                                                                                                                                508 GACAAAATGGATCGAGATGCAATTTATAGTATGTATATAGAAGATATAAGTAACAAAAAT 567
                                                                                                                                                                                                                                                                                              628 ATAGATATAAACAAAAAGAAAAAAAGATATAGATATAGATGTAGACATAGATAAAGAT 687
                                                                                                                                                                                    301 TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT
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APPLICANT. MALLELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1700 Lincoln Street, Suite 3500
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......: US/08/630,822A
N1: APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61, Application US/08630822A Patent No. 5840695 . GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLENN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC.compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CONNELL, GARY J. REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.0%;
nilarity 50.8%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 863-0223 FORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2706 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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688 ATACATA 694
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Best Local Similarity
Matches 93; Conserva'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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US-08-630-822A-61
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AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 240
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Pred. No. 0.01;
0; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/559,896B
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTION: SEQUESTRIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08559896B
Patent No. 6310046
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FORT DETRICK, FREDERICK
MARYLAND
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: Double
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Best Local Similarity
Matches 187; Conserva
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21702-5012
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US-08-559-896B-1
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244 GAACAGAAAGTICAACIGCIICGIAAIIGGCAICAACIICAIGGAAAGAAA	2414 GAACTTAAGGAAGAACTTGAGGAAAAATCTCGTCATATTCAAGAAAGGAAGAAGAAGA 2473	304 GACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAAAATTCAG 363	2474 GAAGGTTGGTTCATCAGCTACAAATTGCATTAGCTAGAGCTGATTCAGAGGCTTTGGCG 2533	364 ACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATC 423	2534 AGATCAATAGATGAAAGTATAGCTGATTTAGAAAAGGAAAAGACTATGAAGGAATTA 2593	424 CAA 426	2594 GAA 2596
24	241	30	2474	364	2534	424	2594
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Search completed: June 15, 2003, 21:13:05 Job time : 66 secs

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Appli
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Sequence 70, Appl
Sequence 35, Appl
Sequence 1, Appli
Sequence 1, Appli
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Watt, Jacqueline
APPLICANT: Whatt, Jacqueline
APPLICANT: Shang, Hong
TITLE CO INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: 85/09 602,669
CURRENT FILING DATE: 2001-63-09
PRIOR PILING DATE: 2000-09/19
PRIOR PLING DATE: 2000-09/19
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Sequence 152, App
Sequence 35, Appl
Sequence 36, Appl
                                                                    Appli
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Sequence 1, Appl
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Sequence 892, App
Sequence 249, App
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Sequence 3002, Ap
Sequence 51, Appl
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Sequence 8652,
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                                                                                                                                                                                                                                                                       US-09-925-637-51
US-08-781-986A-152
US-10-154-221-35
US-10-154-251-36
US-10-154-251-36
US-10-239-676-70
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US-09-938-842A-3002
US-10-084-205-51
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US-09-815-242-8509
US-09-815-242-8509
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US-10-091-438-249
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9 US-09-946-807-1
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Patent No. US20020004490A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-04-12 NUMBER OF SEQ ID NOS: 180 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 102
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18846
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US-09-802-669-102
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LENGTH: 836
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Sequence 99, Appl
Sequence 1, Appli
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Sequence 1, Appli
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/cgn2_6/ptodata/z/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/z/pubpna/USO6_NEW_PUB.seq:*
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ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                       June 15, 2003, 20:47:53 ; Search time 126
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US-09-918-995-15171
US-09-918-995-7395
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Listing first 45 summaries
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Query Match 100.0%; Score 435; DB 10; Best Local Similarity 100.0%; Pred. No. 1.4e-103; Matches 435; Conservative 0; Mismatches 0;
                                                                                                                                            Sequence 1, Application US/09884987 Patent No. US20020102653A1 GENERAL INFORMATION:
                                                                       1185 ATCCAAAGCTTGGTC 1199
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(2352)..(2357)
polyA_site
(2518)..(2532)
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(195)..(242)
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LENGTH: 2534
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US-09-884-987-1
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Pred. No. 1.4e-103;
Mismatches 0;
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APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-2078
CURRENT APPLICATION NUMBER: US/09/949,713
CURRENT FILING DATE: 2001-09-X2
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Patent No. US20020044944A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 435; Conservative 0;
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PRIOR APPLICATION NUMBER: UG/09/19
PRIOR FILING DATE: 11988-11-02
PRIOR APPLICATION NUMBER: PCT/JPS
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                             819 ATCCAAAGCTTGGTC 833
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LENGTH: 2534
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                                                                                                                                                                                                                                                                                 APPLICANT: NAGATA, Shigekazu et al TITLE OF INVENTION: DAM CODING FOR HUMAN CELL SURFACE ANTIGEN FILE REFERENCE: 0.002-48.77 CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: ~2001-06-21
NUMBER OF SEO ID NOS': 11
SOFTWARE: PatentIn/version 3.0
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APPLICANT: Ferrick, David A.
APPLICANT: Ferrick, David A.
APPLICANT: Swift, Susan E.
APPLICANT: Swift, Susan E.
APPLICANT: Armstrong, Randall
APPLICANT: Armstrong, Randall
APPLICANT: Fox, Bryan
TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige
TITLE OF INVENTION: Secretion and Switch Rearrangement
FILE REFERENCE: A-66038 4-7RMS/JUD/DER
CURRENT APPLICATION NUMBER: US 09/076 956, 976A
CURRENT FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VERSION 3.1
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; Pred. No. 2.6e-103;
0; Mismatches 0;
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; Patent No. US20020123076A1
; GENERAL INFORMATION:
                                                                                                                                  ; Sequence 7, Application US/09966976A
; Patent No. US20020168649A1
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100.0%;
                   1211 ATCCAAAGCTTGGTC 1225
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Best Local Similarity 100.(
Matches 435; Conservative
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusaon, Eric G.
APPLICANT: Watt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound
FILE REFRENCE: ISPH-545
CURRENT APPLICATION NUMBER: US 09/802/669
PRIOR FILING DATE: 2001-03/09
PRIOR FILING DATE: 2000-09-48
PRIOR FILING DATE: 2000-09-48
PRIOR FILING DATE: 1999-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
                                                                                                                                Sequence 1, Application US/09802669
Patent No. US20020004490A1
                   NUMBER OF SEQ ID NOS: 180
- SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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Best Local Similarity 100.
Matches 435; Conservative
421 ATCCAAAGCTTGGTC
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LCCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. BIOl. Chem.
VOLUME: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/CURRENT FILING DATE: 2001-05-25
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Armstrong, Randall
                                                                                                     ORGANISM: Artificial sequence
                                   ersion 3.1
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 1998'-05-12
                                                                                                                                       ; OTHER INFORMATION: Synthetic US-09-966-976A-8
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                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Matches 435; Conserva
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SOFTWARE: Patentin ve
SEQ ID NO 8
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 PRIOR FILING DATES
                                 SOFTWARE: Paten
SEQ ID NO 8
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                                                                   LENGTH: 8345
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APPLICANT: Armstrong, Randall
APPLICANT: Fox, Bryan
TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syn
TITLE OF INVENTION: Secretion and Switch Rearrandsment
                                                                 TITLE OF INVENTION: Methods/and Compositions for Screening for Modulators and Ige Syr
TITLE OF INVENTION: Secrétion and Switch Rearrangement
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                                                                                 TITLE OF INVENTION: Secrétion and Switch Rearrangement FILE REFERENCE: A-66039/37/RMS/JJD/DLR CURRENT APPLICATION NUMBER: US/09/963,206B CURRENT FILING DATE: /2001-09/25
                                                                                                                                                                                                                                                                                                                                                              Score 435; DB 10;
Pred. No. 2.6e-103;
; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 435; Conservative 0
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                                 Armstrong, Randall
                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic US-09-963-2068-7
                                                                                                                                   CURRENT FILING DATE: /2001-09
PRIOR APPLICATION NUMBER: US,
PRIOR FILING DATE: 1998-05-27
Ferrick, David A.
                Swift, Susan E
                                                 Fox, Bryan
                                                                                                                                                                                                                                                                          ORGANISM: Artificial
                                                                                                                                                                                       NUMBER OF SEQ ID NOS SOFTWARE: Patentin ve
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TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige TITLE OF INVENTION: Secretion and Switch Rearrangement
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                                                        Gaps
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Length 8345;
                                                     Indels
  100.0%; Score 435; DB 9; 1
100.0%; Pred. No. 2.6e-103;
                                                     0; Mismatches
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; Patent No. US20020123076A1
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                                                                                                                                                                        301 TATGACACATTGATTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTGCAGAGAAATT 360
                                                                                                                                                                                                                                                                            362 TATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAAAATT 421
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122 GAATCTCCAACCTTAGATCCTGAAACAGGCAATAAATTTATCTGATGTTGACTTGAGT 181
                                                    32 AGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACCTTAAATCCTGAAACAGTGG
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                                  121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA
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Pred. No. 2.2e-93;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2490, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
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APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND ITILE OF INVENTION: AND DIAGNOSIS OF PILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(398)
; OTHER INFORMATION: n = A,T,C or
US-09-867-701-2490
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Best Local Similarity 99.5%;
Matches 395; Conservative
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LENGIH: 398
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                                                                                     1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCAT
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              Length 8345;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756 FURRENT APPLICATION NUMBER: US/09/918,995 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR PILING DATE: 1999-01-20 NUMBER OF SEQ ID NOS: 38054 SOFTWARE: FASLEEQ for Windows Version 3.0 SEQ ID NO 17119
                Score 435; DB 10;
Pred. No. 2.6e-103;
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llarity 97.9%; Pred. No. 6.7e-96;
Conservative 0; Mismatches 8
                                                  0; Mismatches
                100.0%; Score 435;
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(490)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17119
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                                al Similarity 100.
435; Conservative
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                Query Match
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Matches 47
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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Watt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR PILING DATE: 2000-09-18
PRIOR PPLICATION NUMBER: US 09/290,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCAATGAAGC 201
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Pred. No. 1.2e-82;
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               CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT APPLICATION NUMBER: US/09/954,531
PRIOR PILLING DATE: 2002-05-02
PRIOR PLILING DATE: 2006-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR PLLING DATE: 2000-09-20
PRIOR PLLING DATE: 2000-09-20
PRIOR PLLING DATE: 2000-09-22
PRIOR PLLING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR PLLING DATE: 2000-09-22
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Patent No. US20020004490A1
GENERAL INFORMATION:
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    Gene Sets
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Matches 354; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-954-531-998
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LENGTH: 1840
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                                                            CCAATCTTTGTACTCTTGCAGAAAATTCAGACTATCATCCTCAAGGACATTACTAGTG
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APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastEQ for Mindows Version 4.0
                                                                                                                                          392 ACTCAGAAATTCAAACTTCAGAAATGAAATCCAAAG 428
                                                                                                                                                                       Score 383.6; DB 10;
Pred. No. 1.6e-90;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                            Sequence 3156, Application US/09867701
Patent No. US20020132237A1
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Best Local Similarity 99.0%;
Matches 386; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapien
US-09-867-701-3156
                                                                                                                                                                                                                                                                        -09-867-701-3156
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134 CTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCA 193
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                                                                                       GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.
TITLE OF INVENTION:
TITLE OF INVENTION:
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100.0%; Pred. No. 3.3e-69;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-918-995-15171
; Sequence 15171, Application US/09918995
; Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(496)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15171
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Matches 302; Conservative
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TC 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 GTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCAATGAAGCCAAAATAGATGATGA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 GTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCA 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 TTTGTACTCTTGCAGAGAAATTCAGACTATCATCATCAAGGACATTACTAGTGACTCAG 397
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                                                                                                                                                                                                                                                                                                                  98 ATTIATCIGATGITGACTIGAGIAAAIAIATCACCACTATIGCIGGAGICAIGACACTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGGTC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 AAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGGTC 423
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Best Local Similarity 100.0%; Pred. No. 3.3e-69;
Matches 302; Conservative 0; Mismatches 0;
                                                                                                                                                                                      Score 330; DB 10;
Pred. No. 3.1e-76;
0; Mismatches 5;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13045
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13045, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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; LCCATION: (1)...(489)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-13045
                                                                                                                                                                                      75.9%;
98.5%;
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Best Local Similarity 98.5
Matches 333; Conservative
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ORGANISM: Homo sapiens
                                                                                           ; LOCATION: (95)...(426)
US-09-802-669-101
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US-09-918-995-13045
                                                                 NAME/KEY: CDS
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OM nucleic - nucleic search, using sw model

June 15, 2003, 19:50:58; Search time 1424 Seconds (without alignments) 4947.357 Million cell updates/sec Run on:

US-09-884-987-1_COPY_765_1199 Title: Perfect score:

Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

16154066 seqs, 8097743376 residues Searched:

Total number of hits satisfying chosen parameters:

32308132

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

em_estba:* EST: * Database :

em_esthum:

em_estmu:

em_estro: em_estov: em_estpl: em_htc:* gb_est1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. em_gss_other:* em_gss_rod:*

em_gss_mam:* :unj_esp_ma

gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:*

em_gss_hum: em_estom:*

			Description	AW994695 RC1-BN003	BQ051037 AGENCOURT	BI254532 602978522	BF126149 601650407	AA180032 2093q12.r	AA293570 zt25h11.r	
SUMMARIES			្ន	AW994695	BQ051037	BI254532	BF126149	AA180032	AA293570	
			DB	10	14	13	12	σ	6	
			Match Length DB ID	1	1055	176	808	398	460	
	æ	Query	Match	9.66	98.8	94.7	93.4	7.06	88.2	
			Score	433.4	429.8	412	406.4	394.4	383.6	
		Result	0	-	7	Ю	4	S	9	

23	57 AV6511			8 AGENCOU				_	0259	AA745982 ob18912.s	BI766250 603052708	AW141.748 EST291827	AJ392468 AJ392468	ALS42092 ALS42092	. ALS66565 ALS66565	AL071063 Drosophil	BJ441951 BJ441951	BJ436174 BJ436174	BJ379111 BJ379111	A2175342 SP_0132_A	AI231531 EST228219	AZ318375 1M0037N07	BJ345089 BJ345089	BJ363187 BJ363187	C90546 C90546 Dict	BJ413360 BJ413360	BJ360248 BJ360248	BJ389689 BJ389689	BJ364065 BJ364065	BJ387004 BJ387004	BJ324059 BJ324059	-	23809	91376	28095 BJ3280	4027 BJ41402	61397 BJ3613	37 BJ4100	
W05802	AV651157	S	AA860068	BM922638	AV715411	•	. H02935	~		AA745982	BI766250	AW141748	AJ392468	AL542092	AL566565			BJ436174			AI231531		BJ345089		C90546	BJ413360 .		BJ389689						9137	280	1402	513	100	
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ALIGNMENTS

RESULT 1 AM994695 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AW994695 RC1-BN0039-060200-011-a05 BN0039 Homo sapiens CDNA, mRNA sequence. AW994695.1 GI:8254929 BST. human. Homo sapiens EURATYOLA: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE AUTHORS	namentary definitions; Catalinini; Nominidae; Nomo. 1 (bases 1 to 509) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,P.H., M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
TITLE JOURNAL MEDLINE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001

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BI254532
602978522F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123477 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAAGGTTCTCAT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAAGGCTTTGTTCGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_71"
/tissue_type="lelomyosarcoma"
/lab host="BH10B (phage-resistant)
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT-Average insert size 2.1 kb.
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 NIH-MGC.http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                     can
                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1055;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 429.8; DB 14; Length
Pred. No. 3.9e-90;
0; Mismatches 2; Indels
                                                                                                                                                                                                                      1. .1055
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5785846"
                                            rausberg, Ph.D.
                                                                                                                                                                                           High quality sequence stop: 689
Location/Qualifiers
                                            Contact: Robert Strausberg, F
Email: cgapbs-rømail.nih.gov
Tissue Prochement: ATCC
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Best Local Similarity 99.5%;
Matches 431; Conservative
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BI254532
BI254532.1 GI:
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BI254532
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                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCl-BN0039-060 200-011-a05&t3=200-02-06&t4=1) Seq primer: puc. 18 forward High quality sequence stop: 509.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUUJIUJ/ 1055 DP MRNA linear EST 29-MAR-2002
AGENCOURT 6954504 NIH_MGC_71 Homo saplens CDNA clone IMAGE:5785846
57, mRNA sequence.
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1055)
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                                                                                                                                                                                                                                                                                                                                        99.6%; Score 433.4; DB 10;
llarity 99.8%; Pred. No. 5.1e-91;
Conservative 0; Mismatches 1;
 Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ051037
BQ051037.1 GI:19810377
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                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I toases 1 to 70°.

NHF-MGC http://mgc.npi.nih.gov/.

National Institutes/of Health, Mammalian Gene Collection (MGC)

Contact: Robort Strausberg, Ph.D.

Emali: cgapba-rémail.nih.gov

Tissue Procurèment: ATCC
                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life machinologies.
                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lnl.gov
http://inage.lnl.gov
Plate: LLAM1301 row: 1 column: 06
High quality sequence stop: 757.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 776;
                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 412; DB 13;
Pred, No. 5.3e-86;
0; Mismatches 0;
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ilarity 99.5%;
Conservative
                Homo sapiens
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RESULT 4 BF126149

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/organism="Homo saplens"
/db_xref='taxon:9606"
/db_xref='taxon:9606"
/clone='InAGE:3934273"
/clone='InAGE:3934273"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: liver: Vector: pDNR-LIB (Clontech); Site_l:
SfiI (gqccgctcggcc); Site_2: SfiI (ggccattaggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGGCC'3' and 3' adaptor sequence:
5'-ATTCTAGGGCGGGCGGCGGCAGCTGTGT(3)BN·3' (where B = A,
C, or G and N = A, C, G, Or T). Average insert size l.85
kb (range l.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BF126149 809 bp mRNA linear EST 24-OCT-2000 601650407F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:3934273 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Repert Strausberg, Ph.D.

Email: cgabbe remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MG clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM774 row: n column: 02
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NIH-WGC http://mgc.nci.nlh.gov/.
National Instructs of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e-84;
0; Mismatches 1;
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Location/Qualifiers
                                                mRNA sequence.
BF126149
BF126149.1 GI:10965189
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99.3%;
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1 (bases 1 to 460).

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, S., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags g70044478
                                                                                                                                                                                                                                                                                                                                                                                                          AA293570 460 bp mRNA linear EST 08-AUG-1997 2L25hll.rl Soares ovary tumor NbHOT Homo sapiens CDNA clone IMAGE:714213 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GGCATCAACATCAAGGAAAGAAGAAGCGTATGACACATTAAAGATCTCAAAAAAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1853 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 125.
Location/Qualifiers
                                                                                          AGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAAGTTCAACTGCTTCGTAATT
                                                                                                                                GGCATCAACTTCATGGAAAGAAGAAGCGTATGACACATTGATTAAAGATCTCAAAAAG
                                                                       MO 63108
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4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
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/clone_11b-"Soares ovary tumor NbHOT"
/sex-"Female"
                                                                                                                                                                                                                                                                               ACTCAGAAAATTCAAACTTCAGAAATGAAATCCAAAG 428
                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
/db_xref-"GDB:5934710"
/db_xref-"taxon:9606"
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Mammalia; Eutheria;
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1 (bases I to 399)

1 (bases I to 509)

1 (bases I to 509)

2 (bases I to 509)

3 (bases I to 509)

4 (bases I to 509)

5 (blistoc, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Miller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., M., Hullman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280400 Muman expressed sequence tags
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                                                                                                                                                                                                       EST 31-DEC-1996
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2093gl2.rl Stratagene ovarian cancer (#937219) Homo sapiens CDNA clone IMAGE:594502 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
                   92 CAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACCACTATTGCTGGAGTCATGA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 CACTARGICAAGITAAAGGCITIGIICGAAAGAATGGIGICAAIGAAGCCAAAATAGATG 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28H13 rev2 from Amersham High quality sequence stop: 263.
361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 ACCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACCTTAAATCCTGAAACAGTGG
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Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 6.1e-82;
0; Mismatches 2;
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/db_xref="taxon:9606"
/clone="IMAGE:594502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
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AA180032.1 GI:1761298
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al Similarity 99.5%;
395; Conservative
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Chinese National Human Genome Center at Shanghai
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In (Dases 1 to 676)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soars, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washur Marck EST Profect
Unpublished (1995)

Contact: Wilson-RK
Washigton Uffiversity School of Medicine
Washigton Uffiversity School of Medicine
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LIML; contact the
IMAGE Consortium (info@dimage.llnl.gov) for further information.
Seq prime: mob.REGA+ER
High quality sequence stop: 307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W05802 676 bp mRNA linear EST 23-APR-1996 za89f05.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299745 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN ); mRNA sequence.
W05802 GI:1278534
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  AACCAAGGTTCTCATGAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCT
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                                               Length 460;
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                                             Score 383.6; DB 9;
Pred. No. 2.1e-79;
0; Mismatches 4;
    ų
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/db_xref="GDB:1244669"
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/clone="IMAGE:299745"
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 81
                                            Query Match
Best Local Similarity 99.0%;
Matches 386; Conservative
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80
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EST 15-JAN-2002
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Xu,X., Huang,J., Xu,Z., Otan,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepstceellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma in those of corresponding noncancerous liver
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 ATATATCACCACTATTGTTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 AGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAG
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U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                                                                                                                                               Query Match 85.1%; Score 370; DB 14; Best Local Similarity 98.0%; Pred. No. 3.2e-76; Matches 395; Conservative 0; Mismatches 6;
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21625106
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Eukaryota; Metazoa;
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AA860068
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1 (bass 1 to 395)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 AAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 bp mRNA linear EST 09-JUN-200 QV4-BF0407-020300-122-d09 BT0407 Homo sapiens CDNA, mRNA sequence. BE070451.1 GI:8415097 EST.
                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                  /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                    /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                             1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAAGGAAAACCAAGGTTCTCAT
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20202663
                                                                                                                                                                                                                                                                                                                  Length 417;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                            Shanghai
                                                                                                                                                                                                                                                                                                               Query Match

81.4%; Score 354; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.6e-72;
Matches 354; Conservative 0; Mismatches 0;
                                                       Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
Location/Qualiflers
                                                                                                                                                                                                                                                                    108
                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCCMD03"
/clone_lib="GLC"
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             201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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                                                                                                                                                                                                                                                                   74 C
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Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-BT0407-020
300-122-d09&t3=2000-03-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 50
High quality sequence stop: 395.
                                                                                                                                                                                                                                                                                                                                                                                                  AA860068 305 bp mRNA linear EST 11-MAR-1998
HGBBT125 Human Glialblastoma Cell Homo sapiens CDNA, MRNA sequence.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Hc
(bases 1 to 305)
Jin, H. L., Hu, S.N., Tu, C., Yuan, J.G. and Olang, B.Q.
DDRT-PCR of Humen Filalblastoma Cell Line BT-325 CDNAs
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 297.8; DB 10;
Pred. No. 2e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 GCGTATGACACATTGATTAAAGATCTCAAAAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 TAGTATGACACATTGATTAAAGATCTCAAATAA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .68.5%; Score 297.8;
llarity 95.5%; Pred. No. 2e-5
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone_lib="BT0407"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                              rel: +55-11-2704922
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Matches 318; Conserv
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                                                                                                                                                                                                                                                               1. 305
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_rofe="Laxon:9606"
/clone_lib="Human Glialblastoma Cell"
/cell_line="BT-325"
/lab_host="E.coll DH5a"
/note="Organ: Brin: Vector: PCRII, Invitrogen; Total RNA was isolated from human glialblastoma cell line BT325
Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell.
Differentially expressed PCR products were cloned and sequenced."
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NIH-MGC http://mocs.nci.nih.gov/.
National Instructes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

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Email: cgapbert/Strausberg, Ph.D.

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Email: cgapbert/Strausberg, Ph.D.

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5', mRNA sequence.
BM922638
BM922638.1'GI:19373017
EST.
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Contact: Bogin Qiang
National Laboratory of Medical Molecular Biology, CAMS & PUMC
National Laboratory of Medical Sciences, Peking Union Medical College (
Chinese Academy of Medical Sciences
5 Dong Dan San Tiao, Beijing 100005, P.R. China
Tel: (010) 55296411
Fax: 8610-524629
Email: zh357&iname.com
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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AV715411 AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5', mRNA sequence. AV715411
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                                                                                                                                                                                                                                                                                                                                //ncte="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV. (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for [Lill-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIMAGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA 180
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 696)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 21
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Pred. No. 1.6e-51;
0; Mismatches 23
                                                                High quality sequence start: 52
High quality sequence stop: 628.
Coation/Qualiflers
                                                                                                                                                                                                                                       /clone="IMAGE:575724"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                          /organism="Homo sapiens'
//db_xref="taxon:9606"
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Best Local Similarity 91.3%;
Matches 337; Conservative
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National Laboratory of Medical Molecular Biology, CAMS & PUMC
Institute of Basic Medical sciences, Peking Union Medical College &
Chinese Academy of Medical Sciences
5 Dong Dan San Tiao, Beijing 100005, P.R. China
Tel: (010)65296411
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HGBBT116 Human Glialblastoma Cell Homo sapiens cDNA, mRNA sequence.
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Jin, H.L., Hu, S. N., Tu, C., Yuan, J.G. and Qiang, B.Q.
DDRT-PCR of Human Glialblastoma Cell Line BT-325 cDNAs
,G., Cheng, Z. and Han, Z.
Homo sapiens CDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoy/Ing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P.R. China
Fax: 86-21-50801929
Ema; 86-21-50801922
Emajá: hanzg@ehgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
141 c 156 g 189 t
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                                                                                                                                                                 Emaj4': hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     DB · 10;
                                                                                                                                                                                                                                                                                                                                                                                                                   ch 46.3%; Score 201.2; DB 10.31 Similarity 98.5%; Pred. No. 7.3e-37; 203; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                   /clone_lib="DCB"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCBAUC01"
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57 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
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Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washu-Warck EST Project
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                     /note="Organ: Brain; Vector: PCRII, Invitrogen; Total RNA was isolated from human gliablastoma cell line BT325. When Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid Induced cell. Differentially expressed PCR products were cloned and public products were cloned and public products were cloned and public products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTÄAAGGCTTTGTTCGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1432 Std Brror: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                  Score 196.4; DB 9; Length 217; Pred. No. 8.2e-36; D; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                       /clone_lib="Human Glialblastoma Cell"
/cell_type="Glialblastoma Cell"
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/db_xref="GDB:563902"
                                                                                /cell_line="BT-325"
/lab_host="E.coli DH5a"
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Location/Qualifiers
'db_xref="taxon:9606"
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Insert Size: 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AAGAATGGTGTCAATGAA 198
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Best Local Similarity 99.5%;
Matches 197; Conservative
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H02935
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IMAGE:151767
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                                                                                                                                                                                 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a fluision of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email:
                                                                      AL542093 ALI_FL002_PL1 Homo sapiens cDNA clone CSODE009106 5 prime
                                                                                                                                                                                                                                                                                                                                                                                                                264 TCGTAATTGGCATCAACTTCATGGAAAGAAAGAAGCGTATGACACATTGATTAAAGATCT 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not and cloned into the Not I and Eco RV sites of the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 932)
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                         Length 461;
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                               /clone_lib="Soares placenta Nb2HP"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Maryland cvc.v, fliang@lifetech.com URL :
http://fulllength.invltrogen.com"
                                                                                                                                                                                                                                                                                                                                      Score 172; DB 14;
Pred. No. 4.4e-30;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 172; Conservative
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AUTHORS
TITLE
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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KEYWORDS
SOURCE
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                                       Gaps
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 Length 932;
                                       Indels
 6
Score 169.4; DB
Pred. No. 2e-29;
1; Mismatches
38.9%;
98.3%;
Query Match 38.9
Best Local Similarity 98.3
Matches 170; Conservative
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Search completed: June 15, 2003, 21:11:49
Job time : 1428 secs

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(without alignments) ' 2749.125 Million cell updates/sec
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1 GWLCLLLLPIPLIVWVKRKE......KANLCTLAEKIQTIILKDIT 145
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                         OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext (
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Maximum DB seq length: 2000000000
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Command line parameters:
-WOOFGL_frame+_LoR.model -DEW-xlp
-WOOFGL_L/USFVO_spool/VS0984987/runat_09062003_140300_13176/app_query.fasta_1.327
-UG-/cg01_1/USFVO_spool/VS0984987/runat_09062003_140300_13176/app_query.fasta_1.327
-DB-GenEmbl .OFWT-fastap -SUFFIX-P2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits .START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-UOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -TRR_MIN_16 -MODE-LOCAL
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Database : GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_ln:*
4: gb_ow:*
5: gb_pat:*
7: gb_pi:*
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10: gb_pi:*
11: gb_st:*
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13: gb_un:*
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15: em_ba:*
16: em_hun:*
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em_vi:*	em_htg_hum:*	em_htg_inv:*	em_htg_other:*	em_htg_mus:*	em_htg_pln:*		em_htg_mam:*	em_htg_vrt:*	em_sy:*	em_htgo_hum:*	em_htgo_mus:*	am htan other.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	7994 H	0519 H.	96	00	e Sequen	3572	173438 Seq	10 CD	121 CDNA	154 Hu	11	7 H.sapiens		5813	41.	o Sedneuc	7 Sednenc	<u>ه</u> :	200000 H.Saplens F	H saniens	: =	H.sapien	3 H.sapien	3 H.sapien	2 Sequence 1	Sequence :	0 Macaca f	0 Macaca n	208	Cercoce		Macaca	Sedneuc	sednence	492 H.Sapien	835 Aotus tr	2357	342 H.sapiens A	384 csnptnfrs	286 н.	57394	21299	AB021296 Oryctolag
SUMMARIES	ID	tn.	HSFAS4DEL	E05336	E35160	A87646	AR163572	3	E05110 .	E09121	HUMFASANT	AR143111		BC012479		AX146814	4 .	AX060542	AX060536	HSFASAPOA	HOFFACIONS	HSFASCESS HSFASCA6DI.	HSFAS346			158632		AB031420	AF344850	AF326208	AF344843	AF344833	AY007572	AX331556	AX336/15	184/	14	2		L G75384	HSFASX9	5739	212	AB021296
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	Result No.														ပ	oʻ																												

ALIGNMENTS

RESULT 1

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Ruberti,G.
Direct Submission
Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R.,
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                                                /note="Not translated in this variant. /number=9
                                                                                                                                                               761
145
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Matches:
Conservative:
Mismatches:
Indels:
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270519.1 GI:1418817
FAS soluble protein; FAS/Apo 1 gene.
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/standard_name="FAS/Apo 1"
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Mammalla; Eutheria; Primates;
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H.sapiens FAS/Apo 1 mRNA
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Best Local Similarity:
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ORIGIN
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                PRI 15-DEC-1997
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Submitted (24.JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,
Immunology, viale C.Marx 43, Rome, Italy, I-00137
2 (bases I to 761)
Cascino, I., Flucci, G., Papoff, G. and Ruberti, G.
Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative spricing
J. Immunol. 154 (6), 2706-2713 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_riet = "SPPRBL: 014294"
/db_riet = "SPPRBL: 014294"
/translation="MLGIWTLIPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
ETQNLEGLHHDGOFCHKPCPPDVNMESSRNAHSPATPSAKRKDPDLTWGGFVFFFCQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name="FAS/Apo 1"
/note="Translated in a different frame in this variant up
to a new stop codon at 310."
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
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/note="Translated in a different frame in this variant."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Alternative splicing variant of FAS gene missing exons 3 and 4. Exons 5 and 6 translated in a different frame up to new stop codon at 310."
                                                                                                                                                                                                                                                                                                                                                       On Mar 25, 1995 this sequence version replaced gi:695540.
Location/Qualifiers
1. 761
                  linear
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/note="Not translated in this variant."
/number=8
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/note="Not translated in this variant.
               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell_type="PHA-activated PBMC" .312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence-experimental
/product="FAS soluble protein"
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/db_xref="G1:695541"
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/standard_name="FAS/Apo 1"
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                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                761 bp
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/db_xref="taxon:9606"
/chromosome="10"
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                       H.sapiens FAS Del 2 mRNA.
247994
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                                                             247994.1 GI:728579
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                                                                                             Homo sapiens.
Homo sapiens
                HSFASCDS2
                                                                              FAS gene
                            DEFINITION
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920 bp mRNA linear PRI 28-NOV-1995
X83490
X83490.1 GI:971454
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ChengyJ., Zhou,T., Lu,C., Shapiro,J.P., Brauer,M.J., Kiefer,M.C.,
Barr,P.J. and Mountz,J.D.
Protection from Fas-mediated apoptosis by a soluble form of the Fas
                                                                                                                                             121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
                                                                                                                                                                                                                                                           81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                           Liu,C., Cheng,J. and Mountz,J.D.
Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Station,
                                                                   LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
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/cell_type="peripheral blood mononuclear cells"
/cell_type="peripheral blood mononuclear cells"
/cene="Fas/Apo-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-DEC-1994) J. Cheng, University of Alabama Birmingham, Division of Clinical Immunol. & Rheum., UAB LHRB 473, Birmingham AL 35294-0007, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 310 (Pt 3), 957-963 (1995)
96013198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /isolate="healthy individual"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q24.1 or 10q23"
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Location/Qualifiers.
1. .920
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/qene="Fas/Apo-1"
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ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
RCRLCDEGHDVNMESSRNAHSPATPSAKRKDPDLTWGGFVFFFCQFH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135. .396
'note="Translated in a different frame in this variant.
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Immunology, viale C.Marx 43, Rome, Italy, I-00137
Location/Qualifiers
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/note="Translated in a different frame
co a new stop codon at 448."
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Matches:
Conservative:
Mismatches:
                                                                                                               /cell_type="PHA-activated PBMC"
1. .450
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/db_xref="GI:1418918"
/db_xref="SPTREMBL:014292"
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'note="Not translated in
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/note="Not translated in
                                           ⁄organism="Homo sapiens"
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179 c 197 g
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/number-2
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/number=1
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Best Local Similarity:
Query Match:
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                               source
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101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
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                                                                                                                                                                          PI HIDEAKI HAGIWARA,YASUYUKI AOTSUKA,JUNICHI MIYAHARA PC
C12115/09,AGIK31/00,A61K48/00,C07K16/42,C07K19/00,C12N5/10, PC
C12N15/02//
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                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1457)
Hadiwara, H., Actsuka, Y. and Miyahara, J.
Method for inducing apoptosis
Patent: JP 2000102389-A 7 11-APR-2000;
YOSHIHIDE HAGIWARA, HIDEAKI HAGIWARA
OS ARTHIGTAL SEQUENCE
PN JP 2000102389-A/7
PD 11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                           243
             1. .1008
/organism="Homo sapiens"
/db_xref="taxon:9606"
. 205 c 217 g 24
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   Location/Qualifiers
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JP 2000102389-A/7.
                                                                                    4.06e-71
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Best Local Similarity:
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                                                                       Alignment Scores:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1008)
                                                                                                                                                                                                    US-09-884-987-2_COPY_175_319 (1-145) x HSFAS34 (1-920)

    .1008
/product='Fas protein'

                                                  Conservative:
Mismatches:
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PAtent: JP 1993219959-A 2 31-AUG-1993;
OSAKA BIO SCI KENKYUSHO
                               Length:
Matches:
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strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1008 bp
DNA encoding human Fas protein.
E05336
E05336 I GI:2173525
JP 1993219959-A/2.
Homo sapiens.
Filter
                                                                       Indels:
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OSRDA JUICHE
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*source: cell_line=KT-3;
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JP 1993219959-A/2
                          3.64e-71
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101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
                                                                                                                                                           717 GGGTGGCTTTGTCTTCTTCTTTTGCCAATTCCACTAATTGTTTGGGTGAAGAAAGGAA 776
                                                                                                                                                                                                                                                                                                            81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                                                                                                                                      GlyTrpLeuCysLeuLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu
                                                                                                                                                                                                                                                                  61 ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                  US-09-884-987-2_COPY_175_319 (1-145) x A87646 (1-2534)
                                         Length:
Matches:
Conservative:
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Magata, S., Itoh, N. and Yonehara, S.
DNA coding for human cell surface
Patent: US 6270998-A 1 07-Aug.-2-01
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                                                                                                                                                                                                                                                                                                                                                 unidentified.
unidentified
unclassified.
1 (bases 1 to 2534)
Screaton, G.R. and Xu, X.
MATERIALS AND METHODS RELATING/TO THE PROTECTION OF USEFUL IMMUNE
                                                                                                                                                                                                                                                                ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
                                                                                                                                                                                                                                                                                                          LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
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Mismatches:
Indels:
                Location/Qualifiers (7): (1317). Location/Qualifiers
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Matches:
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SCREATON GAVIN ROBERT (GB); ISIS IN
Location/Qualiflers
1 2534 inidedtified"
/Organism-"unidedtified"
/db_xref="taxon:32644"
                                                  1. .1457
/organism="unidentified"
/db_xref="taxon:32644"
309 c 340 g 367
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Sequence 4 from Patent WO9835692.
A87646.
A87646.1 GI:6736281
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CTCAAGGACATTACT 1266
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C12R1:91)
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1077 ATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAGAAAATTCAGACTATCATC 1136
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Catarrhini; Hominidae; Homó.
897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGTC
                                                                                                   AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys
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                                           ThrileAlaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySAsnGlyVal
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CIZNI5/12,CIZNI5/85//CIZP21/00,(CIZNI5/12,CIZRI:91),
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1831. .1836
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DNA CODING HUMAN CELL SURFACE ANTIGEN
PATENT: JP 1993184368-A 1 27-JUL-1993;
OSAKA BIO SCI KENYVUSHO
OS HOMO SAPIENS
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195. .242
243. .1199
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*source: cell_line=KT-3;
*source: clone=pF98;
*source is identified by simila
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 487 c 503 g 72
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27-JUL-1993
27-APR-1992 JP 1992107323
26-APR-1991 JP 91P 125234
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E05110
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Location/Qualifiers
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PC (C12P21/00,C12R1:91);
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JP 1993184368-A/1.
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Mammalia; Eutheria;
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                              1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu 20
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                                                         717 GGGTGGCTTTGTCTTCTTTTGCCAATTCCACTAATTGTTTGGGTGAAGAGAAAGGAA
                                                                                    21 ValGinLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
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   US-09-884-987-2_COPY_175_319 (1-145) x AR163572 (1-2534)
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Conservative:
Mismatches:
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Nakamura, N. and Nagata, S.
Fas antigen derivatives
Patent: US 6306395-A 16 23-OCT-2001;
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Sequence 16 from patent US 6306395.
AR173438
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Best Local Similarity:
Query Match:
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Pred. No.:
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1 (bases 1 to 2534):
Itoh, N., Yonehara, S., Ishii, A., Yonehara, M., Mizushima, S., Sameshima, M., Hase, A., Seto, Y. and Nagata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                         Fas antigen; cell surface antigen; transmembrane protein.
Homo sapiens (clone pF58) (tissue library: pCEV4) cDNA to mRNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                    US-09-884-987-2_COPY_175_319 (1-145) x E09121 (1-2534)
/cell_type='cancer c
/cell_line='KT3'
1. 188
189. 1202
/product='hFas'
                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                Matches:
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/organism="Homo sapiens"
                                                         1203. .2534
                                                                                                          /db_xref="taxon:9606"
487 c 503 g
                                                                       Location/Qualifiers
                                                                                                                     503 g
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Cell 66 (2), 233-243 (1991)
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Best Local Similarity:
Query Match:
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1 (Dases 1 to 2534)

1 (Dases 1 to 2534)

Yonehara, S., Kishi, S., Nishimura, K., Yamazaki, Y. and Kobayashi, Y. PRODUCTION OF SOLUBLE MEMBRANE PROTEIN PATENT.
                                                                                                                                                                                                                                                                                                                              PAT 29-SEP-1997
                                                                                                                                                                                                                              AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                                                                                                                                    777 GTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACC 836
                                                                                                                                                                    ValGlaLysThrCysArgLysHisArgLysGluAsnGlaGlySerHisGluSerProThr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF 26-CTT-1993 JP 1993267644
PI YONEHARA SHIN, KISHI SHUJI, NISHIMURA KEIKO, YAMAZAKI
YOSHIAKI, PI KOBAYASHI YUKO
PC C12P21/02,C12N1/21,C12N15/02,C12N15/09,C12P21/08,(C12P21/02,
                                                                                                                       GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu
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strandedness: Double;

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    /organism='Homo sapiens'

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             Length:
Matches:
Conservative:
Mismatches:
Indels:
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JP 1995115988-A/2
                                                                                                US-09-884-987-2_COPY_175_319 (1-145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           topology: Linear;
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CDNA encoding hFas.
E09121
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Homo sapiens
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                                    Percent Similarity:
Best Local Similarity:
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 Alignment Scores:
Pred. No.:
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AUTHORS
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Dean, N.M. and Marcusson, E.G.
Antisense inhibition of Fas mediated signaling
Patent: US 6204055-A 1 20-MAR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSAPO1 2551 bp mRNA line
H.sapiens mRNA for APO-1 cell surface antigen.
X63717
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Mismatches:
Indels:
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                                                                                           AR143111 2551 bp
Sequence 1 from patent US 6204055
AR143111.1 GI:15104397
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493 c 508 g
                                     1137 CTCAAGGACATTACT 1151
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                                                                                                                                                               Unknown.
Unclassified.
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Best Local Similarity:
Query Match:
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Pred. No.:
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ACCESSION
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TITLE
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                                                                                                                                              /product="Fas antigen"
protein_id="AnaA63174.1"
db_xref="GI:189410"
/translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
                                                                                                                                                                                                      RCRLCDEGHGLEVEI NCTRTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGI IKECTLT
SNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPE
                                                                                                                                                                                                                            TVAINLSDVDLSKYITTIACVATLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAECKVQ
LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL
                                                                                                                                                                                            ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
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                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pF58"
           Location/Qualifiers
1. .2534
                                                                            tissue_lib="pCEV4"
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                                                                  /cell_line-"KT3"
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/gene="fas"
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Best Local Similarity:
Query Match:
DB:
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1043 GITCAACTGCTTCGTAATIGGCATCAACTTCATGGAAAGAAAGAAGGATGTGACATIG 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2719)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 28 Row: i Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
                                                  863 TTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC
                                                                                                            LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                                                                                                                                          101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu
                                                                                    ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., G
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="MGC:21432 IMAGE:4514272"
//Lisue_Lype="Bladder, transitional cell papilloma"
//clone_lib="NIH_MGC_93"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens, Similar to tumor necrosis factor receptor superfamily, member 6, clone MGC:21432 IMAGE:4514272, mRNA, complete cds.
BC012479
BC012479.1 GI:15214691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc. CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Tissue Procurement: ATCC
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IVAINLSDVDLSKYITTIAGVWTLSQVKGEVRKNGVNEAKIDEIKNDNVQDTAEQKVQ
LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL
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                                                                                                                                                                                  Submitted (10-FBB-1992) P.H. Krammer, German Cancer Research Center, Tumorimmunology Program, Im Neuenheimer Feld 280, 6900 Heidelberg. FRG

2 (Dases 1 to 2551)

2 (Dases 1 to 2551)

Chan, A., Behrmann, I., Falk, W., Pawlita, M., Maier, G., Li-Weber, M., Richards, S., Dhein, J., Trauth, B.C., Postlangl, H. and Krammer, P. H. Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor Teceptor superfamily. Sequence identity with the Fas antigen J. Biol. Chem. 267 (15), 10709-10715 (1992)
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Krammer, P.H.
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/db_xref="GI:28742"
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LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL
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ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
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Methods and compositions for screening using diphtheria toxin
                                    necrosis factor receptor
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/note="Vector: pCMV-SPORT6"
                        /codon_start=1
/product="Similar to tumor
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/protein_id="AAH12479:1"
/db_xref="G1:15214692"
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Mismatches:
                                            /organism="synthetic construct"
/db_xxef="taxon:32630"
/note="synthetic"
2249 c 2040 g 2101 t
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WO 0134806-A 7 17-MAY-2001;
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           Rigel Pharmaceuticals, Inc. (US)
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C12ScFas survival
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-Q=Cqqn2_1/USPPO_spool/USQ984987/runat_09062003_140300_13165/app_query.fasta_1.327
-Q=Cqqn2_1/USPPO_spool/USQ984987/runat_09062003_140300_13165/app_query.fasta_1.327
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DCALIGN-200 -THR_SCORE=-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15.
-USER-USQ9884987_eCGN_11_208_erunat_09062003_140300_13165 -NCPU-6 -ICPU-3
-NOAMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPLOCK-100 -LONGLOG
-PBV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPORT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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1504.792 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Ygapop 10.0 , Ygapext
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                                                                                                                                                                                                                                                                              4 Human Fas cDNA variants (AAT34527-30) are derived from alternative splicing of Fas gene transcripts. They were identified following PCR amplification of cDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angloimmunoblastic lymphadenopathy (AILD) patients and from healthy subjects. In comparison to the Fas gene (AAT34520), variant Fas del3 (AAT34529) has a deletion of nucleotides 391-637. This deletion causes frame shifting and an altered amino acid sequence (AAR99683).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
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                                                                                                                                                                                                                Natural, soluble form of Fas antigen secreted by human cells result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                Zhou T;
                                                                                                                                                                Liu C, Mountz JD,
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 sig_peptide
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chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation.

(4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA: M2 is useful for careening an agent capable of modulating GCA preferably in an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (MX) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening for an agent capable of modulating GCA or an inflammation (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to detecting (M1) granulocyte (GC) activation
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                                                                                                                                                                                                                                                                                                                                                                    Human cDNA differentially expressed in granulocytic cells #1264
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141 LeuLysAspileThr
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glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection; viral infection, parasitic infection, protozoal infection, fungal infection and M5 is seguence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part

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                                                                                                                                                                                                                                                                           21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
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                                                                                                                                                                                                                                                                                                                  LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                                                                                                                                                                                                            ThrileAlaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySAsnGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE; angioimmunoblastic lymphadenopathy; AILD; ss.
                                                                            of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                     other;
                                                                                                                                                920
145
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                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                  BP; 312 A; 180 C; 186 G; 242 T; 0
                                                                                                                                                Length:
Matches:
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26..1033
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                                                                                                                                                                            Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                    Percent Similarity:
                                                                                                                     Sequence 920
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                                                                                                                                       Alignment Scores
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AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A cDNA clone (AAT34526) codes for a membrane receptor-like protein, Fas antigen (AAR99681). It was isolated from cDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angloimmunoblastic lymphadenopathy (AILD) patients, and from healthy subjects, by PCR amplification. In addition to fascobath 4 other PCR Products were obtd. (see also AAT34527-30). These coded for soluble forms (AAR99682-85) of Fas antigen that are present at higher levels in SLE and AILD patients than the non-soluble Fas
                                                                                                                                                                                                                                                                                                                                                                          is
                                                                                                                                                                                                                                                                                                                                                                       Natural, soluble form of Fas antigen secreted by human cells result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other;
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Mismatches:
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Matches:
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Gaps:
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                                                                                                                                                                                                                                                                                  Zhou T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 A; 231 C;
                                                                                                                                                                                                                                                                                Cheng J, Liu C, Mountz JD,
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/*tag= a
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Best Local Similarity:
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                                                                                                                                                                           22-DEC-1995;
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                sig_peptide
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AAA39167 RESULT

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1012 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAATGGTGT 1071
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41 LeuAsnProGluThrValAlalleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                        ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
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/ _tag= C
/note= "this residue is not present in pF3"
1831..1836
/ *tag= d
1 2352..2357
/ *tag= e
2518..2523
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195...242
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P-PSDB; AAR28084.
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121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
                   The present invention describes a method for causing apoptosis in which a fused gene consisting of a gene participating to apoptosis and a gene encoding at least the variable region of anti-idiotype antibody is transfected to a call to express the fused gene and then an idiotype antibody is reacted with the expressed cell. The method is useful in medical, pharmacoutical in paramaceutical, pharmacological and blochemical fleids. The present sequence encodes a fusion protein designated apoptobody3sc, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                      Apoptobody3sc fusion protein encoding nucleotide sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                         Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
medical; pharmaceutical; pharmacological; biochemical; ds.
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Mismatches:
Indels:
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Matches:
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/product= "apoptobody3sc"
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 7..1317
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                                                                                                                                                                    AAA39167 standard; DNA; 1457 BP
                                                                  141 LeuLysAspileThr 145
                                                                                   968 CTCAAGGACATTACT 982
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(HAGI/) HAGIWARA H.
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                    GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
                                                                     A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The CDNA was ligated to BstXI-out vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS7 cells which were then suspended in buffer containing murine anti-Fas Ab. The cells were panned on plates pre-coated with goat anti-mouse antibodies. The Fas-expressing cells adhered to the plates. Extrachromosomal DNA was prepared from adhered cells and used to transform E.coli VMIO0 cells. A 520bp XhoI-BamHI fragment from a positive clone (PF3) was used to screen the KT-3 cDNA library. The longest cDNA clone was designated pF58 and contains an ORE corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thr I lealaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                                                       2534
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Mismatches:
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Matches:
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                                                 Claim 3; Fig 1 and 2; 27pp; English.
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                                                                                                                                                                                                                                                            Alignment Scores:
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AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                                                                                                                                                Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                             I was used in the construction of an expression vector for don. of recombinant soluble membrane proteins. The proteins used in antibody prodn. for the treatment and prevention of diseases.
                                                                                                                                                                                                                                                                                                                  pF58 which contains the human Fas cDNA.
Plasmid pF58; human Fas cDNA; soluble membrane protein;
          antibody production; diseases; treatment; prevention;
                                                                                                                                                                                                                                                                                                                                                                                other;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                               503 G;
                                                 Location/Qualifiers
195..1202
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100.00%
100.00%
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243..1199
/*tag= c
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195..242
                                                                                                                                                                                                                                                                                                                    plasmid
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P-PSDB; AAR78606.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                   AAQ95297 is the
                                                                                                                                                                                                                                                                                                                                                                               Sequence 2534
                              Homo sapiens
                                                                                                                               JP07115988-A
                                                                                                                                                                        26-OCT-1993;
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RESULT 7 AAT16303

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1017 GTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGAAGCGTATGACACATTG 1076
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                                                                                                                                                                                                                                                                                                                                                                  AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                                                                                                                        1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu
                                                                                                                                                                                   21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                                                                                                                                                                                                                                                                                                                               ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                                                                                                                                                                  LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis regulation; gene therapy; lupus; hepatitis; influenza; HIV;
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                                                            US-09-884-987-2_COPY_175_319 (1-145) x AAT16303 (1-2534)
                    Gaps:
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/product= Fas_antigen
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195..1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Fas antigen; derivative;
treatment; diabetes; arthritis;
apoptosis modulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST
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243..1199
/*tag= c
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Query Match:
DB:
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This sequence represents the coding sequence for the human Fas antigen contained within the plasmid pCEV4/hEas. The soluble Fas antigen is included in the immunoasay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas monoclonal antibody, as well as the standard soluble Fas antigen encoded by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoasay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as
                                                                                                                                                                                                                                                                                                                                                                  Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE; rheumatoid arthritis; serum; systemic lupus erythematosus; ss:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis or systemic lupus erythematosus (SLE)
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Matches:
Conservative:
Mismatches:
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/product- Fas antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hachiya T, Noguchi J, Yonehara S;
                                                                                                                                                                                                      AAT16303 standard; cDNA; 2534 BP
                                                                                                    1137 CTCAAGGACATTACT 1151
                                                                                 141 LeuLysAspileThr 145
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94JP-0154706
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P-PSDB; AAR92528.
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Best Local Similarity:
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06-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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(first entry)

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18-NOV-1998
 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLySGluAlaTyrAspThrLeu 120
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                                                                                                                                                                                                                                                                                                                                                                                        AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                             LeuAsnProGluThrValAlalleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                          Fas antigen derivative containing modified extracellular region has low antigenicity, promotes apoptosis and is useful in treatment off viral and other diseases
                                                                                          The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted).

The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                                                                   Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                        US-09-884-987-2_COPY_175_319 (1-145) x AAV07002 (1-2534)
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Conservative:
Mismatches:
Indels:
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                                                                           Disclosure; Fig 1-2; 102pp; Japanese.
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750.00
100.00%
100.00%
Nakamura N;
                                                                                                                                                                                   virus-infected cells.
                WPI; 1997-558981/51
                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                         P-PSDB; AAW50289
                                                                                                                                                                                                                    Alignment Scores:
Nagata S,
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The present sequence represents a Fas cDNA sequence used in the method-of the invention. The method is concerned with reducing depletion of activated Fas-expressing CD8+ T-jumphocyte killer (TK) cells in an immune cell population which also comprises of Fas-ligand (FasL)-expressing activated CD4+ cells. It involves contacting this immune cell population with an effective amount of an agent (e.g. a soluble Fas-Fc fusion protein) which would interfere with the interaction between Fas and FasL. Therefore, the method is useful for dentifying suitable agents which can reduce depletion of activated Fas-expressing CD8+ TK cells in immune cell populations. Also claimed is the use of the agent in the manufacture of therapeutic compositions. Apoptosis of lymphocytes can be triggered by the interaction of the this interaction, the method described and its preparations can prevent apoptosis of CD8+ TK lymphocytes caused by expression of FasL on expectably the result of CD4+ cells. Such FasL-expression activated CD4+ cells. Such FasL-expression with an immunodeficiency virus e.g., human immunodeficiency virus (HTV) or simian immunodeficiency virus e.g., human immunodeficiency virus (HTV) or simian immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              naintenance/regeneration of cytotoxic T lymphocyte (CTL) activity towards the CD4+ cells infected with the infectious agent, enabling treatment (prophylactic and/or therapeutic) of immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
                                                                   Fasl;
                                                        Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL, CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; Simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
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195..1202
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Alignment Scores:
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                                                                     AAV32993 (1-2534)
     Mismatches:
Indels:
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P-PSDB; AAB19341.
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     Similarity:
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                                                                                                                   The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5 -untranslated region, translational start site, translational termination region or 3'-untranslated region of incletc acid molecules encoding Fas, Fas ligand (Fast), or Fap-1 (Fas associated protein 1, protein tyrosine phosphatase). The antisense compounds are used to inhibit the expression of Fas, Fast or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lung
antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
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Mismatches:
Indels:
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Matches:
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                                                                               Page 71-73; 116pp; English.
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Antisense oligonucleotides
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                                          1 (Fap-1) expression
                                                                                                                                                                                                                                                                                                             cancer or lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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61 ThribalaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySASnGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises combining a candidate bioactive agent, optionally linked to a fusion partner, with a cell comprising a fusion nucleic acid composed of the IL-4 inducible epsilon promoter (see AAZ34932), and a reporter gene, such as the present death gene. The promoter is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising an inducible epsilon promoter-chimeric Fas-IRES-hygromycin-bovine growth hormone poly-A tail placed in vector (12s backwards so that no leaky transcription occurs through the CMV promoter. It is an example of a death gene that provides a nucleic acid that encodes a protein which causes a provides die. The death gene can be used as a reporter gene in methods of the invention used to screen for modulators of IgE synthesis, secretion and switch rearrangement. The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-4 inducible epsilon promoter; immunoglobulin;
IGE; antibody; modulator; screening; human; allergy; therapy;
reporter; Cl2ScFas; survival construct; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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                                                                                                                                                                                                                                                                                                                                                      LeuLysAspIleThr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12ScFas survival construct.
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Chimeric - Bos taurus.
Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAsnProGluThrValAlalleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand or Fas associated protein-1 is useful for inhibiting expression of Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to an antisense compound encoding Fas, Fas ligand, or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated signalling is thought to be immunosuppressive, antiinflammatory, hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were designed to target human Fas. Oligonucleotides were synthesised as chimeric oligonucleotides and are useful for treating an animal having an autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition associated with apoptosis, allograft rejection, or ischemia reperfusion injury. Optionally, the above mentioned conditions are prevented by contacting the allograft with the antisense oligonucleotide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligonucleotides are used in diagnostics, therapeutics, prophylaxis and as research reagents and in kits. The oligonucleotides are also useful for research purposes. The present nucleotide sequence is
cytostatic; vasotropic; hepatitis; cancer; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
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Indels:
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                                                                                                                                                 /product- "Fas HSAP01"
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                                                                                        Location/Qualifiers
221..1228
                                                                                                                                                                                                                                                                                             12-APR-1999; 99US-0290640.
18-SEP-2000; 2000US-0665615.
                                                                                                                                                                                                                                                          09-MAR-2001; 2001US-0802669
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(MARC/) MARCUSSON E G.
(WYAT/) WYATT J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related to human Fas.
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P-PSDB; ABP35562.
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Query Match:
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                                                         Homo sapiens
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Kinsella TM;

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                                                                                                                                       ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                                                                                                                                                      AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys
          Absence of the reporter gene indicates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin E; allergy; therapy; switch rearrangement; vector; fas; survival construct; death gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-4 inducible epsilon promoter; human; IgE; antibody
  presence or absence
                                  Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;
                                                            8282
145
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                                                                                                                       US-09-884-987-2_COPY_175_319 (1-145) x AAZ34938 (1-8282)
                                                                     Matches:
Conservative:
Mismatches:
Indels:
                                                            Length:
then induced with IL-4 or IL-13, and the reporter gene is detected. Absence of th that the agent inhibits the promoter.
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                                                                             Percent Similarity:
Best Local Similarity:
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                                                    Alignment Scores
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                                                                                                                                                                          The present sequence is that of survival construct C12ScFas in which the interleukin-4 inducible epsilon promoter-chimeric Fas(CD95)-internal ribosome entry site-hydromycin-bowine growth hormone polyA tail is placed in the C12s vector backwards so that no leaky transcription occurs through the CMV promoter. Methods of the invention utilise diphtheria toxin for screening purposes, especially for identifying modulators of 1gB synthesis, secretion and switch rearrangement. A claimed method of screening for bloactive agents capable of inhibiting the IL-4 inducible epsilon promoter (see AAF30941), which is involved in 1gE switching, comprises: combining a candidate bloactive agent and a cell that does not endogenously express heparin-binding epidermal growth cactor-like growth factor (HBBGF) and which comprises a fusion nucleic acid comprising the IL-4 inducible epsilon promoter and nucleic acid encoding HBBGF, inducing the promoter with IL-4; adding diphtheria toxin to the cell; and determining whether the cell is dead. Survival constructs carrying a death gene and a dring diphtheria toxin to the cell; and determining whether the cell is dead. Survival constructs carrying a death gene and a dring dentified that prevent the production of 1gE synthesis can be identified that prevent the production of 1gE and reduce or eliminate an allergic response.
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                                                                              Screening for agents capable of inhibiting a promoter, especially interleukin-4 inducible epsilon promoter involved in immunoglobulin production, by using diphtheria toxin constructs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;
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                                                                                                                                                Disclosure; Fig 12A-C; 80pp; English.
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AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100

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4161 AATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACAGCAGCAGAACAGAAA 4102
                                                                                                                                                                                                                                      101 ValGlnLeuLeuArqAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
                21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr.40
                                                                immunoglobulin E; allergy; therapy; switch rearrangement; vector;
Fas; survival construct; death gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-4 inducible epsilon promoter; human; IgE; antibody;
                                                                                                                                                                                                                                                                                                                                             3981 CTCAAGGACATTACT 3967
                                                                                                                                                                                                                                                                                                                                                                                                           AAF30948 standard; DNA; 8345
                                                                                                                                                                                                                                                                                                                               141 LeuLysAspileThr 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises combining a candidate bloactive agent, optionally linked to a fusion partner, with a cell comprising a fusion nucleic acid composed of the Ir-4 inducible epsilon promoter (see AAZ34932), and a reporter gene, such as the present death gene. The promoter is then induced with IL-4 or IL-13, and the presence or absence of the reporter gene is detected. Absence of the reporter gene indicates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of Ahhhh survival construct comprising an inducible epsilon promoter-chimeric Fas (either CD8 or mLyt2)-TRES-hydromycin-bovine growth hormone poly-A tail placed in vector Cl2s backwards so that no leaky transcription occurs through the CMV promoter. It is an example of a death gene that provides a nucleic acid that encodes a protein which causes a cell to die. The death gene can be used as a reporter gene in methods of the invention used to screen for modulators of IgE synthesis, secretion and switch rearrangement. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods, cell lines and vectors for screening for modulators of immunoglobulin E synthesis, secretion and switch rearrangement
                                                                                                                                                                                              IgE; antibody; modulator; screening; human; allergy; therapy; reporter; survival construct; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8345 BP; 1915 A; 2264 C; 2084 G; 2082 T; 0 other;
                                                                                                                                                                                  Interleukin-4 inducible epsilon promoter; immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong R, Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that the agent inhibits the promoter.
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                                                                             AA234939 standard; DNA; 8345 BP
99WO-US10497.
                                                                                                                                                                                                                                                                                                                                                                    98US-0076624
                                                                                                                                28-FEB-2000 (first entry)
                                                                                                                                                        Ahhhh survival construct.
                                                                                                                                                                                                                                  Chimeric - Homo sapiens.
Chimeric - Bos taurus.
Chimeric - Unidentified.
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The present sequence is that of survival construct Ahhhh in which the interleukin-4 inducible epsilon promoter-chimeric Fas(CD8 or mLyt2)-internal ribosome entry site-hygromycin-bovine growth hormone polyA tail is placed in the Cl2s vector backwards so that no leaky transcription occurs through the CMV promoter. Methods of the invention utilise diptheria toxin for screening purposes, especially for identifying modulators of IgE synthesis, secretion and switch rearrangement. A claimed method of screening for
                                                                                                                                                                                                     Screening for agents capable of inhibiting a promoter, especially interleukin-4 inducible epsilon promoter involved in immunoglobulin production, by using diphtheria toxin constructs -
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 13A-C; 80pp; English
                                                                                                        WPI; 2001-335931/35.
Kinsella TM;
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US-09-884-987-2_COPY_175_319 (1-145) x AAZ34939 (1-8345)

8345 145 0 0 0

Conservative: Mismatches: Indels:

Matches:

4.68e-82 750.00 100.00% 100.00%

Best Local Similarity: Percent Similarity:

Score:

Query Match:

Length:

99US-0165189.

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bioactive agents capable of inhibiting the IL-4 inducible epsilon computer (see AAF30941), which is involved in IgE switching, comptrises: combining a candidate bioactive agent and a cell that does not endogenously express heparin-binding epidermal growth factor (HBEGF) and which comprises a fusion in uncleic acid comprising the IL-4 inducible epsilon promoter and a nucleic acid encoding HBEGF; inducing the promoter with IL-4; adding diphtheria toxin to the cell; and determining whether the cell is dead. Survival constructs carrying a death gene and a conspiculation promoter survival cell line. Inhibitors of IgE synthesis can be identified that prevent the production of IgE and reduce or cellminate an allergic response.
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Sequence 8345 BP; 1915 A; 2264 C; 2084 G; 2082 T; 0 other;

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larity: 750.00 Matches: 145 larity: 100.00% Matches: 145 lough Conservative: 0 lough Conservative: 0 lough Matches: 0 lough M		GAAAGAAAGAAGCG	GCATCAACTICATE	GCTTCGTAATTG	GTTCAACT	.4101	ą
Matches: 145 1		lybysbysGluAla	phisGlnLeuHisG	uLeuArgAsnTr	ValGlnLe	101	δλ
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Search completed: June 15, 2003, 22:07:31 Job time: 226 secs

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US-08-611-729A-9
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US-08-11-872-3
US-08-11-872-3
US-09-11-872-3
US-09-11-340-1
US-09-134-001C-1838
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US-09-134-001C-1838
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TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
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               21-017B-149
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US-08-098-327E-45
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FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application PC/TUS9517083 GENERAL INFORMATION:
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APPLICATION NUMBER: USSN
FILING DATE: 23-DEC-1994
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LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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606
2016
2137
2617
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9687
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7176
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Best Local Similarity:
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Sequence 1,
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               GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-290-640-1
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US-08-468-560C-1
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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788 AATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAA 847
                                                                                                                                                                                                                                     907
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APPLICANT: ITOH, Naoto
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR.1994
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
ATONNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Virginity: Vir
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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STRANDEDNESS: double
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CLONE: clone pF58
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LOCATION:
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                                                                                                                                                                                                          ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                                                                                                                                                                        ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
                                                GTACAGAAAACATGCAGAAAGCACAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACC
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                                                                                                   LeuAsnProGluThrValAlaileAsnLeuSerAspValAspLeuSerLysTyrIleThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
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Matches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9517083
GENERAL INFORMATION:
APPLICANT:
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PCT-US95-17083-1
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1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu 20
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              TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE TITLE OF INVENTION: ANTIGEN WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                          ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/468,560C FILING DATE: 06-JUN 1995 CLASSIFICATION: 435
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Mismatches:
Indels:
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Matches:
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NAME: MURBY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFERAX: 703-205-8050
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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243..1199
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1831..1836
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2352..2357
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   YONEHARA,
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ZIP: 22040-0747
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Best Local Similarity:
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US-08-468-560C-1
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by similarity with known sequence or
to an established consensus
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to an established consensus
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. (6270998
GENERAL INFORMATION:
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APPLICANT: ITOH, Naoto
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                                                                                                                                          LOCATION: 1831..1836
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                              NAME/KEY: mat_peptide
LOCATION: 243.1199
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                                                                                                         NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: 2518..2523
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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Best Local Similarity:
Query Match:
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                                      21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
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                                                                                                                                                                                                                                                                           APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                   Sequence 1, Application US/09290640 Patent No. 6204055 GENERAL INFORMATION:
                                                                                                                                                                  1137 CTCAAGGACATTACT 1151
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LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. BIOL. Chem.
VOLUME: 267
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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DATE: 1992-05-25
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                                                                                                                      1077 ATTANAGAICTCANANAGCCANICITIGIACTCTIGCAGAGAAATTCAGACTAICATC 1136
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                                   837 TTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC
                                                               61 ThrileAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
                                                                                LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAGATA, No. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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Conservative:
Mismatches:
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Sequence 16, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     LeuLysAspIleThr 145
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100.008
100.008
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2534
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HUMAN FAS

SECRETED 6 16

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NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH
                                       Sequence 3, Application PC/TUS9517083 GENERAL INFORMATION:
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                          PCT-US95-17083-3
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                                         1103 ATTAAAGATCTCAAAAAAGCCAATCTTTGTACTCTTGCAGAAAATTCAGACTATCATC 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThralaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaTyrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135
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                          ValGlnLeuLeuArgAsnTrpH1sGlnLeuH1sGlyLysLysGluAlaTyrAspThrLeu
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC:1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
                                                                                                                                                                                                                                                                                                                         CONCURRENTLY HEREWITH
                                                                                                                                                                                                                       Sequence 9, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                                                  1163 CTCAAGGACATTACT 1177
                                                                                                                                        LeuLysAspileThr 145
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100.00%
100.00%
88.40%
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 857 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                650 AGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                          US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-3 (1-1104)
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Mismatches:
Indels:
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FILING DALL.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
APPLICATION NUMBER: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PR.
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08444231
Patent No. 5652210
                                                                                                                                                                                                                                                                           663.00
100.00%
100.00%
88.40%
                                                                                                                          LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       linear
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Best Local Similarity:
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16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: ID FOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
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                                                       1059 ATTCAGACTATCATCCTCAAGGACATTACT 1088
                     136 IleGlnThrIleIleLeuLysAspileThr 145
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                                                                                                          US-08-152-443A-18; Sequence 18, Application US/08152443A; Patent No. 5663070
                                                                                                                                                                                                                                                                                                    3: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2
FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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100.00%
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243
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TOPOLOGY: linear
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195..1136
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                         nucleic acid
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Best Local Similarity:
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LOCATION:
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                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/444,231
FILING DATE: 18-MAY-1995
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Mismatches;
Indels:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTOMACE: 15-NOV-1993
REGISTRATION: NUMBER: 33,943
REFENCE/DOCKET NUMBER: 33,943
TELEPHONE: (415) 813-5600
                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
88.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2471 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
243
                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
195..1136
                                  Palo Alto
California
                                                                                                                                                       OPERATING SYSTEM:
                                                                                    94304-1018
                                                                                                                                                                                                                          FILING DATE: 18
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-444-231-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                    STATE:
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	Db 656 GTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAGAAGAAGAAGAAGAAGAAGATTG 715 Oy 121 11eLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGluThrIleIle 140
76 ArglysasnGlyvalasnGlualaLysIleaspGluIleLysasnAspasnValGlnAsp 95 	
96 ThralagluglnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115 	
116 AlatyraspthrLeuileLysAspLeuLysLysAlaasnLeuCysThrLeuAlaGluLys 135 	RESULT 12 US-09-290-640-65 ; Sequence 65, Application US/09290640 ; Patent No. 6204055
136 IleGinThrileIleTeuLysAspileThr 145 	; GENERAL INFORMATION: ; APPLICANT: Dean, Nicholas M. ; APPLICANT: Marcusson, Eric G. ; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
RESULT 11 PCT-US95-17083-5 ; Sequence 5, Application PC/TUS9517083 ; GENERAL INFORMATION:	; FILE REFERENCE: ISPH-0351 ; CURRENT APPLICATION NUMBER: US/09/290,640 ; CURRENT FILING DATE: 1999-04-12 ; NUMBER OF SEQ ID NOS: 85 ; SOFTWARE: Patentin Ver. 2.0
APPLICANT: TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN WIMBER OF SEQUENCES: 16 FINDENT ADDITATION OF SEQUENCES.	; SEQ ID NO 65 ; LENGTH: 1480 ; TYPE: DNA
CORRENT AFFLICATION NUMBER: PCT/US95/17083 FILING DATE: CONCURRENTLY HEREWITH	CONSTRUCTION WAS MUSCULUS FEATURE: NAME/KEY: CDS
CLASSFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/371,263	; LOCATION: (50)(1033) ; PUBLICATION INFORMATION: ; JOURNAL: J. Immunol.
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 975 base pairs TYPE: nucleic acid STRANDEDNESS: single	, VOICH 1297 ; PAGES: 1274-1297 ; DATE: 1992-02-15 ; DATABASE ACCESSION NUMBER: M83649/Genbank ; DATABASE ENTRY DATE: 1994-04-18 US-09-290-640-65
č	Ignment Scores:
. 8e - 63 54 . 50 0 . 69% 3 . 93%	e-31 Length: 14 50 Matches: 69 78 Conservative: 27 28 Mismatches: 43 38 Indels: 5 Gaps: 3
DB: 1 US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-5 (1-975)	US-09-884-987-2_COPY_175_319 (1-145) x US-09-290-640-65 (1-1480) OV 2 TrpLeuCysLeuLeuLeuLeuLeuProlleProLeuIleValTrpValLysArglysGlu 20
1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu 20	. 560
1	21 ValGinLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	617 CGGAAAGAAAGTGCTGGAAAAGGAGACAGGATGACCTGAATCTAGAACC
484 484 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60	Oy 41 LeudanProGluThrYalAla1leAsnLeuSerAspValAspLeuSerLySTyrILeThr 60
	Qy 61 ThrilealaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySAsnGlyVal 80
ThrileAlaGlyValMetThrieuSerGlnValLysGlyPheValArgLysAsnGlyVal	728 AGAATTGCTGAAGACATGACAGGAAGCTAAAAAATTGCTGGGAAAATAACATC
536 ACTATIGCIGGAGICATGACACTAAGICAAGITAAAGGCITIGTIGGAAAGAAIGGIGIC 595 81 ASGGIUALUSILEASGGIUILELVSASDASDASDASDAIGIDASDTHYAJAGIUGIDIVS 100	Qy 81 AsnG uAlarys1leAspGlulleLysasnAspAsnValGlnAspThrAlaGluGlnLys 100
	101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu
101 ValGinLeuLeuArgAsnTrpHisGinLeuHisGlyLysLysGlualaTyrAspThrLeu 120	Db 848 GTCCAGCTGCTCTGTGCTACCAATCTCATGGAAGAAGTGATGCATATTA 907

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121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
                                  908 ATCAAGGGTCTCAAAAAGCCGAATGTCGCAGAACCTTAGATAAATTTCAGGACATGGTC 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --CTIGGAICCGGAGAGCICCCAACG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeuIleValTrpValLysArgLysGlu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GGGGGCTTTTCTTTTTGCCAATTCCACTAATTGTTTGGGTGAAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-15 (1-257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                            SECRETED HUMAN FAS ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSTEM: Windows
FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
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                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                      FILING DATE: CONCURENTLY HEREWITH CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 149, Application US/09221017B Patent No. 6444799
                                                                                                                                                                                  equence 15, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: MORRISON & FOERSTER
755 PAGE MILL ROAD
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99.50
55.00%
55.00%
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                                                                                              |||||||:::
968 CAGAAGGACCTT 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                       141 LeuLysAspIle 144
                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                         APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ercent Similarity:
                                                                                                                                                               -US95-17083-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                      Sequence 15,
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59 IleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsn 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 GlnLysVal---GlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 AspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGln 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ........ValAlaIleAsnLeuSerAspValAspLeuSerLysTyr 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 GlyvalAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGlu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- TTGGGCTGCATGGCCGAGCGCGTCAAG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 LysHisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnProGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-884-987-2_COPY_175_319 (1-145) x US-09-221-017B-149 (1-478)
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: PORYPHYROMONAS GINGIVALIS FEATURE:
                                                                                                                                                   PCT/AU98/01023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 TCCCGTCTCGTTATCGGGGTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 GAGGAGTTGATCCGCGAA 48
                                                                                                                                                                                                                                                                          PELECOMMUNICATION INFORMATION
                     PP1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                             APPLICATION NUMBER: PP291
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/7
                                         30-JAN-1998
                                                                                                                                                              FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                           NAME: Monroy, Gladys H
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.83%
24.60%
10.93%
                                                                                                                                                                                                                                                                                                                                                                                                     478 base pairs
                                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 650-494-0792
PRIOR APPLICATION DATA: APPLICATION NUMBER: F
                                         FILING DATE: 30-JAN-]
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    circular
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circure
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                     TELEFAX:
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-----AAAGAAGAGTCGACTTCCAGACACCCAAGCCATCTTGATAAC--- 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 LyslleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLysVal---Gln 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 ThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnPro 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 GluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThrThrIleAla 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 GlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyValAsnGluAla 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-884-987-2_COPY_175_319 (1-145) x US-08-444-005-14 (1-2268)
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                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                        3: Fish & Richardson P.C.
225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00383/026001
ELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                             CELL DEATH PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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Application US/08444005
                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 2268 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.87%
29.79%
10.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
ORMATION FOR SEQ ID NO:
EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 URRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                        ADDRESSEE: Fish &
                                                                                                                                                               FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-444-005-14
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Db 1897 AIGCTTCAGAAGIGGCTGAIGCGGGAAGGCACCAAAGGGCC 1938
Search completed: June 15, 2003, 22:59:24
Job time: 69 secs
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Sequence 8, Appli Sequence 102, Appl Sequence 17119, A Sequence 2490, Ap

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Sequence:

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Sequence 998, App
Sequence 101, App
Sequence 1117, A
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Sequence 99, Appl
Sequence 91, Appl
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Sequence 6140, App
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Sequence 1140, Appl
Sequence 11, Appl
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Sequence 113, Appl
Sequence 647, Appl
Sequence 14730, A
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TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/19,713
CURRENT FILING DATE: 2001-09-12
PRIOR PAPLICATION NUMBER: US/09/180,100
PRIOR PLING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 09-864 761-1804

US-09-974 300-188

US-09-864 761-20550

US-09-864 761-3784

US-09-815-242-8513

US-09-974-300-3000

US-10-329-960-1

US-09-917-8008-1464

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US-09-961-451A-29
        US-09-770-445-647
US-09-783-066-6
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Matches:
Conservative:
Mismatches:
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US-09-842-552-103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09949713
Patent No. US20020044944A1
GENERAL INFORMATION:
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Percent Similarity:
Best Local Similarity:
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Sequence 1, Appl
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/ cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-884-987-1
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Xgapop 10.0 , Xgar
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext 7
6.0 , Delext 7
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Perfect score:
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Jatabase :

Š. Result

Sequence 1464, Ap

sequence 2, Appl

Appli

Sequence 7040, 1 Sequence 3000, 1 Sequence 1, App

Sequence 188, Apr Sequence 20550, A Sequence 3784, Ap Sequence 8513, Ap

	ery Match: :: -09-884-987-
GlyTrpLeuCysLeuLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu 20	Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProlleProLeulleValTrpVallysArglysGlu
ValGinLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40	Oy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr
LeuasnprogluthrvalalaileasnLeuSeraspyalaspLeuSerLysTyrilethr 60	0y 41 LeuasnProGluThrValalaIleasnLeuSeraspValaspLeuSerLysTyrIleThr
ThrilealaglyvalmetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyval 80	Oy 61 ThrilealaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal
AsnGlualalysileaspGluilelysasnaspasnValGluaspThralaGluGlulys 100	Oy 81 ASNGJUAJALYSIJEASPGJUIJELYSASNASPASNVAJGJNASPTKrAJAGJUGJNLYS
ValGinLeuleuargasnTrpHisGinLeuHisGiyLysLysGiualaTyraspThrLeu 120	Oy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu
IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140 	Oy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle
	Oy 141 LeuLysAspIleThr 145 Db 1137 CTCAAGACATACT 1151
109-884-987-1 109-884-987-1 109-884-987-1 109-884-987-1 109-884-987-1 109-884-987-1 109-884-987-1 109-884-987-1 109-884-987-1 109-884-1	RESULT 3 US-09-802-669-1 ; Sequence 1, Application US/09802669 ; Patent No. US20020004490A1 ; GENERAL INFORMATION: APPLICANT: Dean, Nicholas M. APPLICANT: Warty Jacqueline APPLICANT: Warth Jacqueline APPLICANT: Warth Jacqueline APPLICANT: NUMBER: US 09/865,615 CURRENT APPLICATION NUMBER: US 09/665,615 FRIOR FILING DATE: 2000-09-18 PRIOR FILING DATE: 1999-04-12 NUMBER: OF SEQ ID NOS: 180 SOFTWARE: PatentIn Ver. 2.0 SOFTWARE: PatentIn Ver. 2.0 SOFTWARE: SEATH Homo sapiens FRANTIRE: FRANTIRE: FRANTIRE: FRANTIRE:
	; NAME/KEY: CDS ; LOCATION: (221)(1228) ; PUBLICATION INFORMATION: ; JOURNAL: J. Biol. Chem. ; VOLUME: 267
2534 145 0	; FAGES: 10709-10715 ; DATE: 1992-05-25 ; DATABASE ACCESSION NUMBER: X63717/Genbank ; DATABASE ENTRY DATE: 1996-07-19 US-09-802-669-1

Ouery Match: 0 Gaps: 0 US-09-884-987-2_COPY_175_319 (1-145) x US-09-966-976A-7 (1-8282) OY 1 GlyTrpLeuCysLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu 20 1		81 ASGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Db 4041 ATTAAAGATCTCAAAAAGCCAATCTTGTACTTGCAGAGAAATTCAGACTATCATC 3982 Qy 141 LeuLysasp1leThr 145 Db 3981 CTCAAGGACATTACT 3967 RESULT 5 US-09-963-2068-7/c		Alignment Scores: Alignment Scores: Pred. No.: Score: Score: Fercent Similarity: Rest Local Similarity: 100.00\$ Mismatches: Ouery Match: 100.00\$ Mismatches: 100.00\$
	1 11 11 11 11 11 11 11 1	61 61 923 81 983	Db 1043 GTTCAACTTCGTAATTGCCACCAACGAAGGAGAGGAGGAGGAGGAGGAGGAGGAGG	PBD 1163 CTCAAGGACATACT 1177 RESULT 4 US-09-966-976A-7/C Sequence 7, Application US/09966976A Sequence 7, Application US/09966976A Sequence 7, Application US/09966976A Sequence 7, Application US/09966976A Sequence 7, Application Sequence 1, Application Sequence 1, Application Sequence 1, Application Wethods and Compositions for Secretion and Switch Rearrangement 7 ITLE OF INVENTION: Methods and Compositions for Secretion and Switch Rearrangement 7 ITLE OF INVENTION NUMBER: US/09/966,976A CURRENT Application NUMBER: US/09/966,976A SPRIOR PAPLICATION NUMBER: US/09/966,976A SPRIOR FILING DATE: 1998-05-12 NUMBER OF SEQ ID NOS: 19 SSQ ID NO 7 LENGTH: 8282 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA	FEATURE: OTHER INFORMATION: sy OTHER SCORES: Lignment Scores: ed. No.: ore: Treent Similarity: sst Local Similarity: 1

	US-09-963-206B-8/c ; Sequence 8, Application US/09963206B ; Patent No. US20020123076A1 ; GENERAL INFORMATION: ; APPLICANT: Ferrick, David A. ; APPLICANT: Swift, Susan E. ; APPLICANT: Armstrong, Randall ; APPLICANT: Fox, Bryan ; APPLICANT: Fox INVENTION: Methods and Compositions for Screening for Modulators and Ige	TITLE OF INVENTION: Secretion and Switch Rearrangement FILE REFERENCE: A-66038-3/RMS/JJD/DLR CURRENT APPLICATION NUMBER: US/09/963,206B CURRENT FILING DATE: 2001-09-25 CURRENT FILING DATE: 1998-05-12 PRIOR APPLICATION NUMBER: US 09/076,624 PRIOR PILING DATE: 1998-05-12 NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin version 3.1 SEQ ID NO 8 LENGTH: 8345 TYPE: DNA ORGANISM: Artificial sequence FEATURE: COTHER INFORMATION: Synthetic US-09-963-206B-8	Alignment Scores: Pred. No.: Score: Score: Score: Score: Score: Score: Percent Similarity: Score: Percent Similarity: Score: Sco
GlyTrpLeuCysLeuLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu 20 1 1 1 1 1 1 1 1 1	Oy 141 LeuLysAspileThr 145 Db 3981 CTCAAGGACATTACT 3967 RESULT 6 US-09-966-976A-8/c ; Sequence 8, Application US/09966976A ; Patent No. US20020168649A1	GENERAL INFORMATION: APPLICANT: Swift, Susan E. APPLICANT: Swift, Susan E. APPLICANT: Swift, Susan E. APPLICANT: Fox, Erry and all APPLICANT: Fox, Erry and Compositions for Soreening for Modulators and Ige Syn TITLE OF INVENTION: Methods and Compositions for Soreening for Modulators and Ige Syn TITLE OF INVENTION: Secretion and Switch Rearrangement FILE REFERENCE: A-66038-4/RMS/JJD/DLR FILE REFERENCE: A-66038-4/RMS/JJD/DLR CURRENT FILING DATE: US/09/966,976A CURRENT FILING DATE: 1998-05-12 RIOR APPLICATION NUMBER: US 09/076,624 PRIOR FILING DATE: 1998-05-12 NUMBER OF SEQ ID NOS: 19 SOFTWARE: PatentIn version 3.1 SEQ ID NO 8 SEQ ID NO 8 LENGTH 8345	S-0 1119 rred cor cor esr esr esr esr esr esr esr esr esr es

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239 CGAAAGAATGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGAC 298
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                                                   ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer
                                                                                                                                                                                                                          Sequence 11119, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq. Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFFWARE: FASELSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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LOCATION: (1)...(490)
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OTHER INFORMATION: n
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Best Local Similarity:
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LENGTH: 490.
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US-908-02-05-102.

Sequence 102, Application US/09802669

Patent No. US20020004490al

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M.

APPLICANT: Myatt, Jacqueline

APPLICANT: Thang, Hong

TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

FILE REFERENCE: ISPH-545

CURRENT PELICATION NUMBER: US/09/802,669

PRIOR FILING DATE: 2001-03-09

PRIOR PILING DATE: 2000-09-18

PRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 180

SOFTWARE: Patentin. Ver. 2.0

SEQ ID NO 102

LENGTH: 836
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                                                                                                                                   ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
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 4281 TTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC
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Mismatches:
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Matches:
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Gaps:
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88.40%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-802-669-102
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                                                                                   SEQ ID NO 3156
                                                                                                      LENGTH: 460
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                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 IleLysAsnAspAsnValGlnAspThrAlaGluGlnLysValGlnLeuLeuArgAsnTrp 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 HisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeuIleLysAspLeuLysLysAla 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuSerGlnValLysGlyPheValArgLysAsnGlyValAsnGluAlaLysIleAspGlu 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAla 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 IleAsnLeuSerAspValAspLeuSerLysTyrIleThrThrIleAlaGlyValMetThr 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-884-987-2_COPY_175_319 (1-145) x US-09-867-701-2490 (1-398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
                                                                                                                                           APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THI
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 20121.497
CURRENT FALLIG DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2490
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
.Matches:
.Conservative:
.Mismatches:
.Indels:
Gaps:
                                                                                                 Sequence 2490, Application US/09867701
Patent No. US20020132237A1
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LOCATION: (1)...(398)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                -09-867-701-2490
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Sequence 998, Application US/09954531
| Patent No. US20020165180A1
| Patent No. US20020165180A1
| GENERAL INFORMATION:
| APPLICANT: Weaver, Zoe
| TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using |
| TITLE OF INVENTION: Gene Sets | TITLE OF INVENTION: Gene Sets |
| TITLE OF INVENTION Gene Sets |
| TITLE OF INVENTION Gene Sets |
| TITLE OF INVENTION OF GENE SETS |
| PRIOR PILING DATE: 2000-09-18 |
| PRIOR PILING DATE: 2000-09-20 |
| PRIOR PILING DATE: 2000-09-20 |
| PRIOR PILING DATE: 2000-09-20 |
| PRIOR APPLICATION NUMBER: US/60/234, 539 |
| PRIOR APPLICATION NUMBER: US/60/234, 599 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GGAAAGAAATAATCGTATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AspValAspLeuSerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-884-987-2_COPY_175_319 (1-145) x US-09-867-701-3156 (1-460)
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AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
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                                                                                                                                                                                                                                                                                                                                                                        Length:
                       FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
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US-09-867-701-3156
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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TYPE: DNA
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Fatent No. US20020004490a1

FORENEAL INFORMATION:

APPLICANT: Dean, Nicholas M.

APPLICANT: Myatt, Jacqueline

APPLICANT: Myatt, Jacqueline

APPLICANT: Thang, Hong

TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

FILE REFERENCE: ISPH-545

CURRENT APPLICATION NUMBER: US/09/802,669

FRIOR APPLICATION NUMBER: US 09/665,615

FRIOR FILING DATE: 2000-09-18

FRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                             81 AsnGluAlaLys1leAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                      535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
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                                                                                                                                                                        1 GlyTrpLeuCysLeuLeuLeuLeuLeuProlleProLeulleValTrpValLysArgLysGlu.20
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                                                                                                                                                                                                                                ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
                                                                                                                                                                                                                                                                                                                  -----GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC
                                                                                                                                                                                                                                                                                       41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
                                                                                                                                                                                                    439 GGGTGCCTTTGTTTTTTTCCCAATTCCACTAATTGTTTGGG-----
                                                                                                                                             US-09-884-987-2_COPY_175_319 (1-145) x US-09-954-531-998 (1-975)
                                                        Matches:
Conservative:
Mismatches:
Indels:
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SEQ ID NO 101
LENGTH: 1840
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                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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; LOCATION: (95)
US-09-802-669-101
US-09-954-531-998
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US-09-802-669-101
                               Alignment Scores
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Alignment Scores:

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                                                                                                                                                                                                                                                                                                                     11 GACAATGTCCAAGACACAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AspAsnValGlnAspThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeu
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                                                                                                                      US-09-884-987-2_COPY_175_319 (1-145) x US-09-802-669-101 (1-1840)
                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ThrLeuAlaGluLysIleGlnThrIleIleLeuLysAspIleThr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13045, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
FRIOR FILING DATE: 1999-01-20
              Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
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Matches:
                                                                    Indels:
Length:
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SOFTWARE: FastSEQ for Windows Version 3.0
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LOCATION: (1)...(489)
OTHER INFORMATION: n = A,T,C
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425.00
100.00%
100.00%
56.67%
           465.00
97.89%
96.84%
62.00%
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Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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LysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIleLeu 141
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                                                                                                                                                                                             US-09-918-995-15171

Sequence 15171, Application US/09918995

PUBLICATION OF US-030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative: Mismatches: Indels:
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SOFTWARE: FastSEQ for Windows Version 3.0
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15171
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Best Local Similarity:
Query Match:
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LENGTH: 496
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Search completed: June 15, 2003, 23:50:14 Job time : 139 secs

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BQ051037 1055 bp mRNA linear EST 29-MAR-2002
AGENCOURT_6954504 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5785846
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AA852070 HGBBT116
AK002590 Mus muscu
B1766250 603052708
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BG794187 UTSW_SMID
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 1055)
NIH-WGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AA293570 zt25h11.r
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AUTHORS
TITLE
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KEYWORDS
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-Q-Cgn2_1/12PTO_spool/USO984987/runat_09062003_140300_13188/app_query.fasta_1.327
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-UNITS=bits -START=1 -END-1: MATRIX-bloum62 -TRANS-human40.cd1 -LIST=45
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-USER-USO9884997_eCGN_11_LISTS_Grunat_09062003_140300_13188 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCRESE-0 -WAIT -DSPELOCK=100 -LONGLOG
-FGAPOP=0 -YARREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
                                                                                                      June 15, 2003, 21:50:09; Search time 1418 Seconds (Without alignments) 1656.097 Million cell updates/sec
                                                                                                                                                                                                                     32308132
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                     nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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AV651157.1 GI:9872171
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Best Local Similarity:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NIH_MGC_71"
/tissue_type="lelomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyTrpLeuCysLeuLeuLeuLeuDrolleProLeulleValTrpValLysArgLysGlu 20
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                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12873 row: j column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                             Average insert size 2.1 kb.
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Matches:
                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5785846"
              Ph.D.
                                                                                                                                       High quality sequence stop: 689
Location/Qualifiers
           Contact: Robert Strausberg, P
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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EUARATORS METAZOA: Chordata; Craniata; Vertebrata; Euteleostomi; EUARATORS, MetaZOA: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)

2 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao, H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Lii,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Shen,K., Lu,G., Cheng,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

L Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                                                                                                                   Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrilealaGlyValMetThrLeuSerGlnValLySGlyPheValArgLySAsnGlyVal
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                                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801920:
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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/db_xref="taxon:9606"
/clone="GLCCMD03"
/clone_lib="GLC"
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BI254532 17-JUL-2001
602978522F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123477 5',
                                                                                                      ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115
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                                                                                                                                                                                                                                                                      134 AGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 776)
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      SerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal
                                                                                      ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1301 row: 1 column: 06
High quality sequence stop: 757.
Location/Qualifiers
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/lab_host="DH10B"
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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
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/db_xref="taxon:9606"
/clone="IMAGE:5123477"
/clone_lib="NIH_MGC_12"
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Contact: Robert Strausberg, Ph.D.
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Fax: +55-11-2707001

Bmail: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-BN0039-060
200-011-a05&t3=2000-02-06t4=1)
Seq primer: puc 18 forward

High quality sequence stop: 509.

Location/Qualifiers
                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 509)

1 (bases 1 to 509)

1 Abaso, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da.Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F.; Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelare, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: breast_normal; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
                                                                                                  EST 05-JUN-2000
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RCI-BN0039-060200-011-a05 BN0039 Homo saplens CDNA, MRNA sequence.
AW994695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                    roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="BN0039"
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W05802 676 bp mRNA linear EST 23-APR-1996 za89f05.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299745 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN W05802
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASDGIUAIALYSI1eASPGIUIIeLYSASDASPASDASDVAIGIDASPThrAlaGIUGINLYS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratories (Palo Alto
                                                                                                                                                                                                                      LeuAsnProGluThrValAlalleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       School of Medicine vay, Box 8501, St. Louis,
               CA). Note: this is a NIH_MGC Library.
                                                                                       809
140
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   constructed by
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Washington University School
4444 Forest Park Parkway, Box
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/lab_host="DH10B (TI phage-resistant)"
/ncle="Otogan: liver; Vector: pDNR-LiB (Clontech); Site_1:
/ncle="Otogan: liver; Vector: pDNR-LiB (Clontech); Site_1:
Sill (ggcgctcggcc); Site_2: Sill (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTATAGGCGCGACGATG-4T(30)BN-3' (Where B = A,
c' or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb): 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF126149 809 bp mRNA linear EST 24-OCT-2000 601650407F1 NIH_MGC_76 Homo sapiens CDNA clone IMAGE:3934273 5', mRNA sequence.
BF126149
                                                                                                                                                                                                                                                                                                                                   sValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLe 120
233
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. CONSORTIUM (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM774 row: n coluum: 02
High quality sequence stop: 635.
Location/Qualifiers
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:3934273"
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLys
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                                                                                                                                                                                                                                                                                                           9 others
                                                                                                          /clone="IMAGE:299745"
/clone=lib="Soares_fetal_lung_NbHL19W"
/dev.statge="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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BE070451.1 GI:8415097
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                                                                       /organism="Homo sapiens"
/db_xref="GDB:1244669"
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                      Seq primer: mob.REGA+ET
High quality sequence stop: 307
Location/Qualifiers
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/dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mrNA and cDNA amplification were performed under low
stringency conditions.

a 81 c 67 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=6t2-0V4-BT0407-020 300-122-d096t3=2000-03-026t4=1)
Seq primer: puc 18 forward High quality sequence start: 50 High quality sequence stop: 395.
                                                                                Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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20202663
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases.1. to 395)
                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rug Prof. Antonio Prudente 109, 4 andar, 01509-010,
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/clone_lib="BT0407"
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Fax: +55-11-2707001
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dierrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, S., Morts, M., Parsons, J., Pange, C., Rifkin, L., Rohlfing, T., Gohelhenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags groups are sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA180032 2093912.rl Stratagene ovarian cancer (#937219) Homo gapiens CDNA clone INACE:594502 5' similar to 9b:M67454 FASL RECEPTOR PRECURSOR
                                             ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAla---TyrAspThr 119
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: estëwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 263.
Location/Qualifiers
clone_lib="Stratagene ovarian cancer (#937219)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Conservative:
Mismatches:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:594502"
                                                                                                                                                                                                       398 bp
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AA180032
AA180032.1 GI:1761298
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                    human.
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AUTHORS
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HisArgLysGluAşnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAla 47

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BUKATYOCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (base. I to 460).

Hillier, L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, S., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schallenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 bp mRNA 11near EST 08-AUG-1997 tumor NbHOT Homo sapiens cDNA clone to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
                                                      182
                                                                                                                                                                                                               88 IleLysAsnAspAsnValGlnAspThrAlaGluGlnLysValGlnLeuLeuArgAsnTrp 107
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                                                                                                                                          87
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infe@image.llnl.gov) for further information.
Insert Length: 1853 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                       183 ATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAAGTTCAACTGCTTCGTAATTGG
                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:5934710"
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Location/Qualifiers
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/clone="IMAGE:714213"
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IMAGE:714213 5' similar
);, mRNA sequence.
AA293570
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA860068 305 bp mRNA linear EST 11-WAR-1998
HGBBT125 Human Glialblastoma Cell Homo sapiens cDNA, mRNA sequence.
AA860068
                                                                                                                                                                                                                                                                                                                                     240
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Jin, H.L., Hu,S.N., Tu,C., Yuan,J.G. and Qiang,B.O.
DDRT-PCR of Human Glialblastoma Cell Line BT-325 cDNAs
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                         181 AATGTCCAAGACACAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCAT
                                                                                                                                                                                                                        AsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSer
                                                                                                                                                                                                                                        52 AspValAspLeuSerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnVal
 pT7T3
sites of a modified p
constructed by Bento
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/db_xref="taxon:9606"
/clone_lib="Human Glialblastoma Cell"
/cell_type="Glialblastoma Cell"
/cell_tine="BT-325"
/lab_host="E.Coli DH5a"
                                                                                                                                                                                               US-09-884-987-2_COPY_175_319 (1-145) x AA293570 (1-460)
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
the Not I and Eco RI
(Pharmacia). Library
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                           M.Fatima Bonaldo.
                                          81
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Fax: 8610-5240529
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                                                                                                                                         Best Local Similarity:
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                                                                                                                          Percent Similarity:
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                                                                                   Alignment Scores:
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AGENCOURT_6652776 NIH_MGC_118 Homo saplens cDNA clone IMAGE:5755724 BM922638
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1152)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp 95
was isolated from human glialblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell. Differentially expressed PCR products were cloned and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu
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Contact: Robert Strausberg, Ph.D.
Email: capbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                      Mismatches:
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/clone_lib="NIH_MGC_118"
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/db_xref="taxon:9606"
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High quality sequence stop: 628
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Query Match:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 696)
Xu,X., Gu,J., Liu,F.; Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
Homo saptens, cDNA DCB clones
             /note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECCRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NHLMGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        587 AGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 ThralaGlu-GlnLysValGlnLeuLeuArgAsnTrp-HisGlnLeuHisGlyLys---L 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCAGAAACAGAAAGTICCACTGCITICCAATIGGGCATCAACTICATGGGAAAGGAA 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLysTyrlleThrThrlleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp 95
                                                                                                                                                                                                                                                                                                                                                                                                                                         HisGluSerProThrLeuAsnProGluThrValAlalleAsnLeuSerAspValAspLeu 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV715411 AV715411 DCB HOMO Sapiens CDNA clone DCBAUC01 5', mRNA sequence. AV715411 AV715411. GI:10796928
                                                                                                                                                                                                                                                                                                                                                                       US-09-884-987-2_COPY_175_319 (1-145) x BM922638 (1-1152)
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Mismatches:
Indels:
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/lab_host-"DH10B"
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AL542093 AL542093 LT_FL002_PL1 Homo sapiens cDNA clone CS0DE009YI06 5 prime AL542093
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Uni,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                         /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
141 c 156 g 189 t
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BP 191 91006 EVRY cedex - France
Emall: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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82
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                                                at CHGC in Shanghai.
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Mismatches:
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Matches:
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/db_xref="taxon:9606"
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/clone_lib="LTI_FL002_PL1"
                                                                                           /organism="Homo saplens"
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/clone="ncBAUC01"
/clone_lib="DCB"
/cell_type="dendritic cell
/dev_stage="mature"
/lab_host="BM25.8"
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualiflers
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426.00
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Best Local Similarity:
Query Match:
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         /note="Organ: placenta; Vector: pcMvSpORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpORT 6 vector. Library was constructed by Life Technologies. Contact: Freq Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville division of Invitrogen 9800 Medical Center Drive Rockville filang@lifetech.com.URL:
filang@lifetech.com.URL:
210 c 233 g 218 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 bp mRNA linear EST 06-MAR-1996
HGBBT116 Human Glialblastoma Cell Homo sapiens CDNA, mRNA sequence.
AA852070
AA852070.1 GI:2939608
EST.
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Mational Laboratory of Medical Molecular Biology, CAMS & PUMC
Mational Laboratory of Medical sciences, Peking Union Medical College
Chinese Academy of Medical Sciences
S Dong Dan San Tiao, Beljing 100005, P.R. China
Tel: (010)65296411
Fax: 8610-5240529
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens Eutrazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 217) and 213, H.L., Hu.S.N., Tu.C.; Yuan,J.G. and Qiang,B.Q. DDRT-PCR of Human Glialblastoma Cell Line BT-325 CDNAs Unpublished (1997)
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/db_xref="taxon:9606"
/clome_lib="Human Gilalblastoma Cell"
/cell_type="Glialblastoma Cell"
/cell_lipe="Br-325"
/lab_host="E.coli DH5a"
/note="Organ: Brain; Vector: PCRII, Invitrogen; Total
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Mismatches:
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/lab_host-"DH10B
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                                                                                                                                                                                                                                9.32e-35
375.00
98.68%
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Best Local Similarity:
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Pred. No .
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AK002590 1437 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610012D23:tumor necrosis factor receptor superfamily, member 6, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 196
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
was isolated from human glialblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinolc Acid induced cell. Differentially expressed PCR products were cloned and sequenced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mismatches:
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AK002590.1 GI:12832683
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Best Local Similarity:
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us-09-884-987-2_copy_175_319.p2n.rst

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Length:
Matches:
Conservative:
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/db_xref="GI:12832684"
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1437
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291 c 323
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/gene="Tnfrsf6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9216,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lease visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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Genome Res. 10 (11), 1757-1771 (2000) 20530913
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